

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 27, 2006, 03:55:23 ; Search time 894 Seconds  
(without alignments)  
1335.249 Million cell updates/sec

Title: US-10-070-415a-37\_COPY\_410\_430  
Perfect score: 21  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 2842172563 residues  
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_in.\*
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- 4: gb\_om.\*
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- 13: gb\_vi.\*
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- 15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	581	6	BD178531 Method of
2	21	100.0	581	6	BD182924 Detection
3	20	95.2	581	6	BD178510 Method of
4	20	95.2	581	6	BD178511 Method of
5	20	95.2	581	6	BD178512 Method of
6	20	95.2	581	6	BD178513 Method of
7	20	95.2	581	6	BD182903 Detection
8	20	95.2	581	6	BD182904 Detection
9	20	95.2	581	6	BD182905 Detection
10	20	95.2	581	6	BD182906 Detection
11	19.4	92.4	581	6	BD090451 Carrier f
12	19.4	92.4	581	6	BD090452 Carrier f
13	19.4	92.4	581	6	BD090453 Carrier f
14	19.4	92.4	581	6	BD090454 Carrier f
15	19.4	92.4	581	6	BD090746 Polymorph
16	19.4	92.4	581	6	BD090747 Polymorph
17	19.4	92.4	581	6	BD090748 Polymorph
18	19.4	92.4	581	6	BD090749 Polymorph

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 C 93 16.8 80.0 786 13 AF065677 AF065677 Stealth v  
 C 94 16.8 80.0 872 13 AF065662 AF065662 Stealth v  
 C 95 16.8 80.0 1030 5 AF186021 AF186021 Carassius  
 C 96 16.8 80.0 1344 1 X78541 E.coli (O11  
 C 97 16.8 80.0 1972 6 AR642915 Sequence  
 C 98 16.8 80.0 1972 15 BT009556 Triticum  
 C 99 16.8 80.0 2976 15 AY343340 Chlamydom  
 C 100 16.8 80.0 4134 6 CS071660 Sequence

## ALIGNMENTS

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 DEFINITION Method of detecting nucleic acid relating to disease.  
 ACCESSION BD178531  
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 KEYWORDS WO 02077281-A/37.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
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 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.  
 1 (bases 1 to 581)  
 Hashimoto, K., Hashimoto, M., Mishi, S. and Ota, Y.  
 Method of detecting nucleic acid relating to disease  
 Patent: WO 02077281-A 37 03-OCT-2002;  
 TOSHIBA CORP, KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO,  
 YASUHIKO OTA  
 OS Homo sapiens (human)  
 PN WO 02077281-A/37  
 PD 03-OCT-2002  
 PF 05-MAR-2002 WO 2002JP002030  
 PR 27-MAR-2001 JP 01P 090053, 18-SEP-2001 JP 01P 284112 PI  
 KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO, YASUHIKO OTA PC  
 C12Q1/68, C12N15/09, C12M1/00, G01N33/53, G01N33/543, G01N33/566, PC  
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 DEFINITION Detection of nucleic acid associated with disease.  
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 VERSION BD182924.1 GI:31875124  
 KEYWORDS JP 200235083-A/37.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.

REFERENCE 1 (bases 1 to 581)  
 AUTHORS Hashimoto, K., Hashimoto, M., Mishi, S. and Ota, Y.  
 TITLE Detection of nucleic acid associated with disease  
 JOURNAL Patent: JP 200235083-A 37 10-DEC-2002;  
 TOSHIBA CORP  
 COMMENT OS Homo sapiens (human)  
 PN JP 200235083-A/37  
 PD 10-DEC-2002  
 PF 26-MAR-2002 JP 2002086681  
 PI KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO, YASUHIKO OTA PC  
 C12N15/09, C12N15/00, C12M1/00, C12Q1/68, G01N33/53, G01N33/566, PC  
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 VERSION BD178510.1 GI:30015776  
 KEYWORDS WO 02077281-A/16.  
 SOURCE Homo sapiens (human)  
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 Hominidae; Homo.  
 1 (bases 1 to 581)  
 Hashimoto, K., Hashimoto, M., Mishi, S. and Ota, Y.  
 Method of detecting nucleic acid relating to disease  
 Patent: WO 02077281-A 16 03-OCT-2002;  
 TOSHIBA CORP, KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO,  
 YASUHIKO OTA  
 OS Homo sapiens (human)  
 PN WO 02077281-A/16  
 PD 03-OCT-2002  
 PF 05-MAR-2002 WO 2002JP002030  
 PR 27-MAR-2001 JP 01P 090053, 18-SEP-2001 JP 01P 284112 PI  
 KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO, YASUHIKO OTA PC  
 C12Q1/68, C12N15/09, C12M1/00, G01N33/53, G01N33/543, G01N33/566, PC  
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ACCESSION BD178511
VERSION BD178511.1 GI:30015777
KEYWORDS WO 02077281-A/17.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
AUTHORS Hashimoto, K., Hashimoto, M., Mishiro, S. and Ota, Y.
TITLE Method of detecting nucleic acid relating to disease
JOURNAL Patent: WO 02077281-A 17 03-OCT-2002;
TOSHIBA CORP, KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO,
YASUHIKO OTA
COMMENT OS Homo sapiens (human)
PN WO 02077281-A/17
PD 03-OCT-2002
PF 05-MAR-2002 WO 2002JP002030
PR 27-MAR-2001 JP 01P 090053, 18-SEP-2001 JP 01P 284112 PI
KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO, YASUHIKO OTA PC
C12Q1/68, C12N15/09, C12M1/00, G01N33/53, G01N33/543, G01N33/566, PC
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PC G01N37/00
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DEFINITION Method of detecting nucleic acid relating to disease.
ACCESSION BD178512
VERSION BD178512.1 GI:30015778
KEYWORDS WO 02077281-A/18.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
AUTHORS Hashimoto, K., Hashimoto, M., Mishiro, S. and Ota, Y.
TITLE Method of detecting nucleic acid relating to disease
JOURNAL Patent: WO 02077281-A 18 03-OCT-2002;
TOSHIBA CORP, KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO,
YASUHIKO OTA
COMMENT OS Homo sapiens (human)
PN WO 02077281-A/18
PD 03-OCT-2002
PF 05-MAR-2002 WO 2002JP002030
PR 27-MAR-2001 JP 01P 090053, 18-SEP-2001 JP 01P 284112 PI
KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO, YASUHIKO OTA PC
C12Q1/68, C12N15/09, C12M1/00, G01N33/53, G01N33/543, G01N33/566, PC
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DEFINITION Method of detecting nucleic acid relating to disease.
ACCESSION BD178513
VERSION BD178513.1 GI:30015779
KEYWORDS WO 02077281-A/19.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
AUTHORS Hashimoto, K., Hashimoto, M., Mishiro, S. and Ota, Y.
TITLE Method of detecting nucleic acid relating to disease
JOURNAL Patent: WO 02077281-A 19 03-OCT-2002;
TOSHIBA CORP, KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO,
YASUHIKO OTA
COMMENT OS Homo sapiens (human)
PN WO 02077281-A/19
PD 03-OCT-2002
PF 05-MAR-2002 WO 2002JP002030
PR 27-MAR-2001 JP 01P 090053, 18-SEP-2001 JP 01P 284112 PI
KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO, YASUHIKO OTA PC
C12Q1/68, C12N15/09, C12M1/00, G01N33/53, G01N33/543, G01N33/566, PC
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DEFINITION Method of detecting nucleic acid relating to disease.
ACCESSION BD178513
VERSION BD178513.1 GI:30015779
KEYWORDS WO 02077281-A/19.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
AUTHORS Hashimoto, K., Hashimoto, M., Mishiro, S. and Ota, Y.
TITLE Method of detecting nucleic acid relating to disease
JOURNAL Patent: WO 02077281-A 19 03-OCT-2002;
TOSHIBA CORP, KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO,
YASUHIKO OTA
COMMENT OS Homo sapiens (human)
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PD 03-OCT-2002
PF 05-MAR-2002 WO 2002JP002030
PR 27-MAR-2001 JP 01P 090053, 18-SEP-2001 JP 01P 284112 PI
KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO, YASUHIKO OTA PC
C12Q1/68, C12N15/09, C12M1/00, G01N33/53, G01N33/543, G01N33/566, PC
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DEFINITION Detection of nucleic acid associated with disease.
ACCESSION  BD182903
VERSION     BD182903.1  GI:31875103
KEYWORDS   JP 2002355083-A/16.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
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            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominiidae; Homo.
REFERENCE  1 (bases 1 to 581)
AUTHORS   Hashimoto,K., Hashimoto,M., Mishiro,S. and Ota,Y.
TITLE     Detection of nucleic acid associated with disease
JOURNAL   Patent: JP 2002355083-A 16 10-DEC-2002;
TOSHIBA CORP
COMMENT   OS Homo sapiens (human)
          PN JP 2002355083-A/16
          PD 10-DEC-2002
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DEFINITION Detection of nucleic acid associated with disease.
ACCESSION  BD182904
VERSION     BD182904.1  GI:31875104
KEYWORDS   JP 2002355083-A/17.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
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            Hominiidae; Homo.
REFERENCE  1 (bases 1 to 581)
AUTHORS   Hashimoto,K., Hashimoto,M., Mishiro,S. and Ota,Y.
TITLE     Detection of nucleic acid associated with disease
JOURNAL   Patent: JP 2002355083-A 17 10-DEC-2002;
TOSHIBA CORP
COMMENT   OS Homo sapiens (human)
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DEFINITION Detection of nucleic acid associated with disease.
ACCESSION  BD182905
VERSION     BD182905.1  GI:31875105
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SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
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REFERENCE  1 (bases 1 to 581)
AUTHORS   Hashimoto,K., Hashimoto,M., Mishiro,S. and Ota,Y.
TITLE     Detection of nucleic acid associated with disease
JOURNAL   Patent: JP 2002355083-A 18 10-DEC-2002;
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DEFINITION Detection of nucleic acid associated with disease.
ACCESSION  BD182906
VERSION     BD182906.1  GI:31875106
KEYWORDS   JP 2002355083-A/19.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
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            Hominiidae; Homo.
REFERENCE  1 (bases 1 to 581)
AUTHORS   Hashimoto,K., Hashimoto,M., Mishiro,S. and Ota,Y.
TITLE     Detection of nucleic acid associated with disease
JOURNAL   Patent: JP 2002355083-A 19 10-DEC-2002;
TOSHIBA CORP
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          PN JP 2002355083-A/19
          PD 10-DEC-2002
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            PC G01N33/576/(C12Q1/68,C12R1/93),C12N15/00,C12N15/00 CC
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Db 410 GCAAGTGCTGNAGTGGCGGG 430

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 581)  
Hashimoto, K., Hashimoto, M., Mishiro, T., Ota, H., and Hashimoto, K.  
Detection of nucleic acid associated with disease  
Patent: JP 2002335083-A 19 10-DEC-2002;  
TOSHIBA CORP  
OS Homo sapiens (human)  
PN JP 2002335083-A/19  
PD 10-DEC-2002  
PF 26-MAR-2002 JP 2002086681  
PI KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO, YASUHIKO OTA PC  
C12N15/09, C12N15/00, C12Q1/68, G01N33/53, G01N33/566, PC  
G01N33/569,  
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DEFINITION  
Carrier for detecting gene, and its use for detecting efficacy of  
interferon therapy.  
ACCESSION  
BD090451.1 GI:22636061  
VERSION  
BD090451.1  
KEYWORDS  
JP 2001333786-A/1.  
SOURCE  
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ORGANISM  
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 581)  
Tsuchikata, M., Mishiro, T., Ota, H. and Hashimoto, K.  
Carrier for detecting gene, and its use for detecting efficacy of  
interferon therapy  
Patent: JP 2001333786-A 1 04-DEC-2001;  
TOSHIBA CORP  
OS Homo sapiens (human)  
PN JP 2001333786-A/1  
PD 04-DEC-2001  
PF 06-MAR-2001 JP 2001062372  
PI MINAKO TSUCHIKATA, TOSHIHARU MISHIRO, HIROHIKO OTA, KOJI PI  
HASHIMOTO  
PC C12N15/09, C12M1/00, C12M1/34, C12Q1/68, G01N33/53, G01N33/566, PC  
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interferon therapy.  
ACCESSION  
BD090453  
VERSION  
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KEYWORDS  
JP 2001333786-A/3.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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Hominidae; Homo.  
1 (bases 1 to 581)  
Hashimoto, M., Hashimoto, M., Mishiro, T., Ota, H., and Hashimoto, K.  
Detection of nucleic acid associated with disease  
Patent: JP 2002335083-A 19 10-DEC-2002;  
TOSHIBA CORP  
OS Homo sapiens (human)  
PN JP 2002335083-A/19  
PD 10-DEC-2002  
PF 26-MAR-2002 JP 2002086681  
PI KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO, YASUHIKO OTA PC  
C12N15/09, C12N15/00, C12Q1/68, G01N33/53, G01N33/566, PC  
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Detection of nucleic acid associated with disease FH Key  
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Carrier for detecting gene, and its use for detecting efficacy of  
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ACCESSION  
BD090453  
VERSION  
BD090453.1 GI:22636063  
KEYWORDS  
JP 2001333786-A/3.

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Db 410 GCAAGTGTGTAGTGGCGGG 430  
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DEFINITION  
Carrier for detecting gene, and its use for detecting efficacy of  
interferon therapy.  
ACCESSION  
BD090452.1 GI:22636062  
VERSION  
BD090452.1  
KEYWORDS  
JP 2001333786-A/2.  
SOURCE  
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ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 581)  
Tsuchikata, M., Mishiro, T., Ota, H. and Hashimoto, K.  
Carrier for detecting gene, and its use for detecting efficacy of  
interferon therapy  
Patent: JP 2001333786-A 2 04-DEC-2001;  
TOSHIBA CORP  
OS Homo sapiens (human)  
PN JP 2001333786-A/2  
PD 04-DEC-2001  
PF 06-MAR-2001 JP 2001062372  
PI MINAKO TSUCHIKATA, TOSHIHARU MISHIRO, HIROHIKO OTA, KOJI PI  
HASHIMOTO  
PC C12N15/09, C12M1/00, C12M1/34, C12Q1/68, G01N33/53, G01N33/566, PC  
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PC C12N15/00  
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RESULT 13  
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DEFINITION  
Carrier for detecting gene, and its use for detecting efficacy of  
interferon therapy.  
ACCESSION  
BD090453  
VERSION  
BD090453.1 GI:22636063  
KEYWORDS  
JP 2001333786-A/3.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE 1 (bases 1 to 581)  
AUTHORS Tsuchikata,M., Mishiro,T., Ota,H. and Hashimoto,K.  
TITLE Carrier for detecting gene, and its use for detecting efficacy of  
interferon therapy  
JOURNAL Patent: JP 2001333786-A 3 04-DEC-2001;  
TOSHIBA CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2001333786-A/3  
PD 04-DEC-2001  
PF 06-MAR-2001 JP 2001062372  
PI MINAKO TSUCHIKATA, TOSHIHARU MISHIRO, HIROHIKO OTA, KOJI PI  
HASHIMOTO  
PC C12N15/09, C12M1/00, C12M1/34, C12Q1/68, G01N33/53, G01N33/566, PC  
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LOCUS Carrier for detecting gene, and its use for detecting efficacy of  
DEFINITION interferon therapy.  
ACCESSION BD090454  
VERSION BD090454.1 GI:22636064  
KEYWORDS JP 2001333786-A/4.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE 1 (bases 1 to 581)  
AUTHORS Tsuchikata,M., Mishiro,T., Ota,H. and Hashimoto,K.  
TITLE Carrier for detecting gene, and its use for detecting efficacy of  
interferon therapy  
JOURNAL Patent: JP 2001333786-A 4 04-DEC-2001;  
TOSHIBA CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2001333786-A/4  
PD 04-DEC-2001  
PF 06-MAR-2001 JP 2001062372  
PI MINAKO TSUCHIKATA, TOSHIHARU MISHIRO, HIROHIKO OTA, KOJI PI  
HASHIMOTO  
PC C12N15/09, C12M1/00, C12M1/34, C12Q1/68, G01N33/53, G01N33/566, PC  
G01N37/00,  
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CC Carrier for detecting gene, and its use  
for detecting efficacy

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DEFINITION BD090746  
ACCESSION BD090746.1 GI:22636356  
VERSION JP 2001333785-A/1.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE 1 (bases 1 to 581)  
AUTHORS Tsuchikata,M., Mishiro,T., Ota,H. and Hashimoto,K.  
TITLE Polymorphic gene of MxA protein and use thereof  
JOURNAL Patent: JP 2001333785-A 1 04-DEC-2001;  
TOSHIBA CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2001333785-A/1  
PD 04-DEC-2001  
PF 06-MAR-2001 JP 2001062371  
PI MINAKO TSUCHIKATA, TOSHIHARU MISHIRO, HIROHIKO OTA, KOJI PI  
HASHIMOTO  
PC C12N15/09, A01K67/027, A61K31/7088, A61K35/76, A61K48/00, A61P15/00, PC  
A61P25/00,  
PC A61P27/02, A61P27/16, A61P31/12, A61P31/20, A61P31/22, A61P35/00,  
PC A61P35/02,  
PC A61P43/00, C12N5/10, C12Q1/68, C12Q1/70, C12N15/00, C12N5/  
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CC Polymorphic gene of MxA protein and use thereof FH Key  
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LOCUS	BD090747	581 bp	DNA	linear	PAT 27-AUG-2002
DEFINITION	Polymorphic gene of MxA protein and use thereof.				
ACCESSION	BD090747				
VERSION	BD090747.1	GI:22636357			
KEYWORDS	JP 2001333785-A/2.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS	Tsuchikata, M., Mishiro, T., Ota, H. and Hashimoto, K.				
TITLE	Polymorphic gene of MxA protein and use thereof				
JOURNAL	Patent: JP 2001333785-A 2 04-DEC-2001;				
COMMENT	TOSHIBA CORP OS Homo sapiens (human) PN JP 2001333785-A/2 PD 04-DEC-2001 PF 06-MAR-2001 JP 2001062371 PI MINAKO TSUCHIKATA, TOSHIHARU MISHIRO, HIROHIKO OTA, KOJI PI HASHIMOTO PC C12N15/09, A01K67/027, A61K31/7088, A61K35/76, A61K48/00, A61P15/00, PC A61P25/00, A61P27/02, A61P27/16, A61P31/12, A61P31/20, A61P31/22, A61P35/00, PC A61P35/02, PC A61P43/00, C12N5/10, C12Q1/68, C12Q1/70, C12N15/00, C12N5/00 CC Polymorphic gene of MxA protein and use thereof FH Key Location/Qualifiers FT source 1..581 FT Location/Qualifiers 1..581 /organism="Homo sapiens (human)" /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"				
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DEFINITION	Polymorphic gene of MxA protein and use thereof.				
ACCESSION	BD090748				
VERSION	BD090748.1	GI:22636358			
KEYWORDS	JP 2001333785-A/3.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS	Tsuchikata, M., Mishiro, T., Ota, H. and Hashimoto, K.				
TITLE	Polymorphic gene of MxA protein and use thereof				
JOURNAL	Patent: JP 2001333785-A 3 04-DEC-2001;				
COMMENT	TOSHIBA CORP OS Homo sapiens (human) PN JP 2001333785-A/3 PD 04-DEC-2001 PF 06-MAR-2001 JP 2001062371 PI MINAKO TSUCHIKATA, TOSHIHARU MISHIRO, HIROHIKO OTA, KOJI PI HASHIMOTO PC C12N15/09, A01K67/027, A61K31/7088, A61K35/76, A61K48/00, A61P15/00, PC A61P25/00, A61P27/02, A61P27/16, A61P31/12, A61P31/20, A61P31/22, A61P35/00, PC A61P35/02, PC A61P43/00, C12N5/10, C12Q1/68, C12Q1/70, C12N15/00, C12N5/00 CC Polymorphic gene of MxA protein and use thereof FH Key Location/Qualifiers FT source 1..581 FT Location/Qualifiers 1..581 /organism="Homo sapiens (human)" /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"				

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DEFINITION	Polymorphic gene of Mxa protein and use thereof.
ACCESSION	BD090749
VERSION	BD090749.1 GI:22636359
KEYWORDS	JP 2001333785-A/4.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
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	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
	Hominidae; Homo.
REFERENCE	1 (bases 1 to 581)
AUTHORS	Tsuchikata M., Mishiro T., Ota H. and Hashimoto K.
TITLE	Polymorphic gene of Mxa protein and use thereof
JOURNAL	Patent: JP 2001333785-A 4 04-DEC-2001;
COMMENT	TOSHIBA CORP
	OS Homo sapiens (human)
	PN JP 2001333785-A/4
	PD 04-DEC-2001
	PF 06-MAR-2001 JP 2001062371
	PI MINAKO TSUCHIKATA, TOSHIHARU MISHIRO, HIROHIKO OTA, KOJI FI
	HASHIMOTO
	PC
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PC	A61P35/02,
PC	A61P43/00,C12N5/10,C12Q1/68,C12Q1/70,C12N15/00,C12N5/00
CC	Polymorphic gene of Mxa protein and use thereof FH Key
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Query Match 92.4%; Score 19.4; DB 6; Length 581;	
Best Local Similarity 95.2%; Pred. No. 83;	
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	1 GCAAGTCTGTAGTGGGG 21
Db	410 GCAAGTCTGAGTGGGG 430

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RESULT 19
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LOCUS          BD178532          581 bp      DNA      linear      PAT 16-APR-2003
DEFINITION     Method of detecting nucleic acid relating to disease.
ACCESSION      BD178532
VERSION        BD178532.1 GI:30015798
KEYWORDS       WO 02077281-A/38.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
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               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Hominidae; Homo.
REFERENCE      1 (bases 1 to 581)
AUTHORS       Hashimoto,K., Hashimoto,M., Mishiro,S. and Ota,Y.
TITLE         Method of detecting nucleic acid relating to disease
JOURNAL       Patent: WO 02077281-A 38 03-OCT-2002;
               TOSHIBA CORP,KOJI HASHIMOTO,MICHIE HASHIMOTO,SHUNJI MISHIRO,
               YASUHIKO OTA
COMMENT       OS Homo sapiens (human)
               PN WO 02077281-A/38
               PD 03-OCT-2002
               PF 05-MAR-2002 WO 2002JP002030
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               KOJI HASHIMOTO,MICHIE HASHIMOTO,SHUNJI MISHIRO,YASUHIKO OTA PC
               C1201/68,C12N15/09,C12M1/00,G01N33/53,G01N33/543,G01N33/566, PC
               G01N33/576
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ORIGIN
Query Match          92.4%; Score 19.4; DB 6; Length 581;
Best Local Similarity 95.2%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCAAGTCTGTAGTGGCGGG 21
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Db

RESULT 20
BD178533
LOCUS          BD178533          581 bp      DNA      linear      PAT 16-APR-2003
DEFINITION     Method of detecting nucleic acid relating to disease.
ACCESSION      BD178533
VERSION        BD178533.1 GI:30015799
KEYWORDS       WO 02077281-A/39.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
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REFERENCE      1 (bases 1 to 581)
AUTHORS       Hashimoto,K., Hashimoto,M., Mishiro,S. and Ota,Y.
TITLE         Method of detecting nucleic acid relating to disease
JOURNAL       Patent: WO 02077281-A 39 03-OCT-2002;
               TOSHIBA CORP,KOJI HASHIMOTO,MICHIE HASHIMOTO,SHUNJI MISHIRO,
               YASUHIKO OTA
COMMENT       OS Homo sapiens (human)
               PN WO 02077281-A/39
               PD 03-OCT-2002
               PF 05-MAR-2002 WO 2002JP002030
               PR 27-MAR-2001 JP 01P 090053,18-SEP-2001 JP 01P 284112 PI
               KOJI HASHIMOTO,MICHIE HASHIMOTO,SHUNJI MISHIRO,YASUHIKO OTA PC
               C1201/68,C12N15/09,C12M1/00,G01N33/53,G01N33/543,G01N33/566, PC
               G01N33/576
               PC G01N37/00
               CC Method of detecting nucleic acid relating to disease FH Key
               FT source
               FT 1.581
               Location/Qualifiers
               /organism="Homo sapiens (human)"
               /mol_type="genomic DNA"
               /db_xref="taxon:9606"

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Query Match          92.4%; Score 19.4; DB 6; Length 581;
Best Local Similarity 95.2%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCAAGTCTGTAGTGGCGGG 21
        |||||||
        410 GCAAGTCTGTAGTGGCGGG 430

Db

RESULT 20
BD178533
LOCUS          BD178533          581 bp      DNA      linear      PAT 16-APR-2003
DEFINITION     Method of detecting nucleic acid relating to disease.
ACCESSION      BD178533
VERSION        BD178533.1 GI:30015799
KEYWORDS       WO 02077281-A/39.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Hominidae; Homo.
REFERENCE      1 (bases 1 to 581)
AUTHORS       Hashimoto,K., Hashimoto,M., Mishiro,S. and Ota,Y.
TITLE         Method of detecting nucleic acid relating to disease
JOURNAL       Patent: WO 02077281-A 39 03-OCT-2002;
               TOSHIBA CORP,KOJI HASHIMOTO,MICHIE HASHIMOTO,SHUNJI MISHIRO,
               YASUHIKO OTA
COMMENT       OS Homo sapiens (human)
               PN WO 02077281-A/39
               PD 03-OCT-2002
               PF 05-MAR-2002 WO 2002JP002030
               PR 27-MAR-2001 JP 01P 090053,18-SEP-2001 JP 01P 284112 PI
               KOJI HASHIMOTO,MICHIE HASHIMOTO,SHUNJI MISHIRO,YASUHIKO OTA PC
               C1201/68,C12N15/09,C12M1/00,G01N33/53,G01N33/543,G01N33/566, PC
               G01N33/576
               PC G01N37/00
               CC Method of detecting nucleic acid relating to disease FH Key
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Best Local Similarity 95.2%; Pred. No. 83;
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        410 GCAAGTCTGTAGTGGCGGG 430

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C1201/68,C12N15/09,C12M1/00,G01N33/53,G01N33/543,G01N33/566, PC
G01N33/576,
PC G01N37/00
CC Method of detecting nucleic acid relating to disease FH Key
Location/Qualifiers
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Best Local Similarity 95.2%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCAAGTCTGTAGTGGCGGG 21
        |||||||
        410 GCAAGTCTGTAGTGGCGGG 430

Db

RESULT 21
BD178534
LOCUS          BD178534          581 bp      DNA      linear      PAT 16-APR-2003
DEFINITION     Method of detecting nucleic acid relating to disease.
ACCESSION      BD178534
VERSION        BD178534.1 GI:30015800
KEYWORDS       WO 02077281-A/40.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Hominidae; Homo.
REFERENCE      1 (bases 1 to 581)
AUTHORS       Hashimoto,K., Hashimoto,M., Mishiro,S. and Ota,Y.
TITLE         Method of detecting nucleic acid relating to disease
JOURNAL       Patent: WO 02077281-A 40 03-OCT-2002;
               TOSHIBA CORP,KOJI HASHIMOTO,MICHIE HASHIMOTO,SHUNJI MISHIRO,
               YASUHIKO OTA
COMMENT       OS Homo sapiens (human)
               PN WO 02077281-A/40
               PD 03-OCT-2002
               PF 05-MAR-2002 WO 2002JP002030
               PR 27-MAR-2001 JP 01P 090053,18-SEP-2001 JP 01P 284112 PI
               KOJI HASHIMOTO,MICHIE HASHIMOTO,SHUNJI MISHIRO,YASUHIKO OTA PC
               C1201/68,C12N15/09,C12M1/00,G01N33/53,G01N33/543,G01N33/566, PC
               G01N33/576
               PC G01N37/00
               CC Method of detecting nucleic acid relating to disease FH Key
               FT source
               FT 1.581
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Query Match          92.4%; Score 19.4; DB 6; Length 581;
Best Local Similarity 95.2%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCAAGTCTGTAGTGGCGGG 21
        |||||||
        410 GCAAGTCTGTAGTGGCGGG 430

Db

RESULT 22
BD182925
LOCUS          BD182925          581 bp      DNA      linear      PAT 17-JUN-2003

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DEFINITION Detection of nucleic acid associated with disease.
ACCESSION BD182925
VERSION BD182925.1 GI:31875125
KEYWORDS JP 2002355083-A/38.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 581)
Hashimoto, K., Hashimoto, M., Mishiro, S. and Ota, Y.
Detection of nucleic acid associated with disease
Patent: JP 2002355083-A 38 10-DEC-2002;
TOSHIBA CORP
OS Homo sapiens (human)
PN JP 2002355083-A/38
PD 10-DEC-2002
PF 26-MAR-2002 JP 2002086681
PI KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO, YASUHIKO OTA PC
G01N33/569,
PC G01N33/576/(C12Q1/68, C12R1:93), C12N15/00, C12N15/00 CC
Detection of nucleic acid associated with disease FH Key
Location/Qualifiers
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ORIGIN
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Best Local Similarity 95.2%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 21
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Db 410 GCAAGTGTCTAGGTGCGGG 430

RESULT 24
BD182927
LOCUS BD182927 581 bp DNA linear PAT 17-JUN-2003
DEFINITION Detection of nucleic acid associated with disease.
ACCESSION BD182927
VERSION BD182927.1 GI:31875127
KEYWORDS JP 2002355083-A/40.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 581)
Hashimoto, K., Hashimoto, M., Mishiro, S. and Ota, Y.
Detection of nucleic acid associated with disease
Patent: JP 2002355083-A 40 10-DEC-2002;
TOSHIBA CORP
OS Homo sapiens (human)
PN JP 2002355083-A/40
PD 10-DEC-2002
PF 26-MAR-2002 JP 2002086681
PI KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO, YASUHIKO OTA PC
G01N33/569,
PC G01N33/576/(C12Q1/68, C12R1:93), C12N15/00, C12N15/00 CC
Detection of nucleic acid associated with disease FH Key
Location/Qualifiers
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FEATURES
source
Location/Qualifiers
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ORIGIN
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Best Local Similarity 95.2%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 21
|||||
Db 410 GCAAGTGTCTAGGTGCGGG 430

RESULT 23
BD182926
LOCUS BD182926 581 bp DNA linear PAT 17-JUN-2003
DEFINITION Detection of nucleic acid associated with disease.
ACCESSION BD182926
VERSION BD182926.1 GI:31875126
KEYWORDS JP 2002355083-A/39.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 581)
Hashimoto, K., Hashimoto, M., Mishiro, S. and Ota, Y.
Detection of nucleic acid associated with disease
Patent: JP 2002355083-A 39 10-DEC-2002;
TOSHIBA CORP
OS Homo sapiens (human)
PN JP 2002355083-A/39
PD 10-DEC-2002
PF 26-MAR-2002 JP 2002086681
PI KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO, YASUHIKO OTA PC
G01N33/569,
PC G01N33/576/(C12Q1/68, C12R1:93), C12N15/00, C12N15/00 CC
Detection of nucleic acid associated with disease FH Key
Location/Qualifiers
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FEATURES
source
Location/Qualifiers
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/mol_type='genomic DNA'
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ORIGIN
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Best Local Similarity 95.2%; Pred. No. 83;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 21
|||||
Db 410 GCAAGTGTCTAGGTGCGGG 430

RESULT 25
AR441761
LOCUS AR441761 581 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 1 from patent US 6667155.
ACCESSION AR441761
VERSION AR441761.1 GI:42667980
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
1 (bases 1 to 581)
Hijikata, W., Mishiro, S., Ota, Y. and Hashimoto, K.
Carrier for gene detection and its use for detecting validity of
interferon therapy
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JOURNAL Patent: US 6667155-A 1 23-DEC-2003;  
Kabushiki Kaisha Toshiba; Kawasaki;  
JPX;

FEATURES  
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ORIGIN

Query Match 92.4%; Score 19.4; DB 6; Length 581;  
Best Local Similarity 95.2%; Pred. No. 83;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTGCTGTAGTGGCGGG 21  
|||||  
Db 410 GCAAGTGCTGMAGGTGGCGGG 430

RESULT 26  
AR441762  
LOCUS AR441762 581 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 2 from patent US 6667155.  
ACCESSION AR441762  
VERSION AR441762.1 GI:42667981  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 581)  
AUTHORS Hijikata,M., Mishiro,S., Oota,Y. and Hashimoto,K.  
TITLE Carrier for gene detection and its use for detecting validity of interferon therapy  
JOURNAL Patent: US 6667155-A 2 23-DEC-2003;  
Kabushiki Kaisha Toshiba; Kawasaki;  
JPX;

FEATURES  
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ORIGIN

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Qy 1 GCAAGTGCTGTAGTGGCGGG 21  
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Db 410 GCAAGTGCTGMAGGTGGCGGG 430

RESULT 27  
AR441763  
LOCUS AR441763 581 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 3 from patent US 6667155.  
ACCESSION AR441763  
VERSION AR441763.1 GI:42667982  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 581)  
AUTHORS Hijikata,M., Mishiro,S., Oota,Y. and Hashimoto,K.  
TITLE Carrier for gene detection and its use for detecting validity of interferon therapy  
JOURNAL Patent: US 6667155-A 3 23-DEC-2003;  
Kabushiki Kaisha Toshiba; Kawasaki;  
JPX;

FEATURES  
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ORIGIN

Query Match 92.4%; Score 19.4; DB 6; Length 581;  
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Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTGCTGTAGTGGCGGG 21  
|||||  
Db 410 GCAAGTGCTGMAGGTGGCGGG 430

RESULT 28  
AR441764  
LOCUS AR441764 581 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 4 from patent US 6667155.  
ACCESSION AR441764  
VERSION AR441764.1 GI:42667983  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 581)  
AUTHORS Hijikata,M., Mishiro,S., Oota,Y. and Hashimoto,K.  
TITLE Carrier for gene detection and its use for detecting validity of interferon therapy  
JOURNAL Patent: US 6667155-A 4 23-DEC-2003;  
Kabushiki Kaisha Toshiba; Kawasaki;  
JPX;

FEATURES  
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ORIGIN

Query Match 92.4%; Score 19.4; DB 6; Length 581;  
Best Local Similarity 95.2%; Pred. No. 83;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTGCTGTAGTGGCGGG 21  
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Db 410 GCAAGTGCTGMAGGTGGCGGG 430

RESULT 29  
AR577621  
LOCUS AR577621 581 bp DNA linear PAT 14-DEC-2004  
DEFINITION Sequence 1 from patent US 6783935.  
ACCESSION AR577621  
VERSION AR577621.1 GI:56580247  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 581)  
AUTHORS Hijikata,M., Mishiro,S., Oota,Y. and Hashimoto,K.  
TITLE Genetic polymorphism of MxA protein and use thereof  
JOURNAL Patent: US 6783935-A 1 31-AUG-2004;  
Kabushiki Kaisha Toshiba; Kawasaki;  
JPX;

FEATURES  
source Location/Qualifiers  
1. .581  
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/mol\_type="genomic DNA"

ORIGIN

Query Match 92.4%; Score 19.4; DB 6; Length 581;  
Best Local Similarity 95.2%; Pred. No. 83;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTGCTGTAGTGGCGGG 21  
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Db 410 GCAAGTGCTGMAGGTGGCGGG 430

RESULT 30



AR577622  
LOCUS AR577622 581 bp DNA linear PAT 14-DEC-2004  
DEFINITION Sequence 2 from patent US 6783935.  
ACCESSION AR577622  
VERSION AR577622.1 GI:56580248  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 581)  
AUTHORS Hijikata, M., Mishiro, S., Oota, Y. and Hashimoto, K.  
TITLE Genetic polymorphism of MxA protein and use thereof  
JOURNAL Patent: US 6783935-A 2 31-AUG-2004;  
Kabushiki Kaisha Toshiba; Kawasaki;  
JPX;  
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Query Match 92.4%; Score 19.4; DB 6; Length 581;  
Best Local Similarity 95.2%; Pred. No. 83;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GCAAGTCTGTAGTGGCGGG 21  
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Db 410 GCAAGTCTGTAGTGGCGGG 430  
RESULT 31  
LOCUS AR577623 581 bp DNA linear PAT 14-DEC-2004  
DEFINITION Sequence 3 from patent US 6783935.  
ACCESSION AR577623  
VERSION AR577623.1 GI:56580249  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 581)  
AUTHORS Hijikata, M., Mishiro, S., Oota, Y. and Hashimoto, K.  
TITLE Genetic polymorphism of MxA protein and use thereof  
JOURNAL Patent: US 6783935-A 3 31-AUG-2004;  
Kabushiki Kaisha Toshiba; Kawasaki;  
JPX;  
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Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GCAAGTCTGTAGTGGCGGG 21  
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Db 410 GCAAGTCTGTAGTGGCGGG 430  
RESULT 32  
LOCUS AR577624 581 bp DNA linear PAT 14-DEC-2004  
DEFINITION Sequence 4 from patent US 6783935.  
ACCESSION AR577624  
VERSION AR577624.1 GI:56580250  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 581)  
AUTHORS Hijikata, M., Mishiro, S., Oota, Y. and Hashimoto, K.

TITLE Genetic polymorphism of MxA protein and use thereof  
JOURNAL Patent: US 6783935-A 4 31-AUG-2004;  
Kabushiki Kaisha Toshiba; Kawasaki;  
JPX;  
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source Location/Qualifiers  
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Query Match 92.4%; Score 19.4; DB 6; Length 581;  
Best Local Similarity 95.2%; Pred. No. 83;  
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QY 1 GCAAGTCTGTAGTGGCGGG 21  
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Db 410 GCAAGTCTGTAGTGGCGGG 430  
RESULT 33  
LOCUS HSMXAP 1899 bp DNA linear PRI 09-SEP-2004  
DEFINITION H.sapiens DNA for MxA promoter.  
ACCESSION X55639  
VERSION X55639.1 GI:456344  
KEYWORDS MxA promoter.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Chang, K.C., Hansen, E., Foroni, L., Lida, J. and Goldspink, G.  
TITLE Molecular and functional analysis of the virus- and  
interferon-inducible human MxA promoter  
JOURNAL Arch. Virol. 117 (1-2), 1-15 (1991)  
PUBMED 1706589  
REFERENCE 2 (bases 1 to 1899)  
AUTHORS Chang, K.C.  
TITLE Direct Submission  
JOURNAL Submitted (18-SEP-1990) Chang K.-C., The Royal Veterinary College,  
University of London, Royal College Street, London NW1 0TU, U K  
FEATURES  
source Location/Qualifiers  
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115..178  
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promoter  
581..589  
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exon 1583..1681  
/number=2  
ORIGIN  
Query Match 92.4%; Score 19.4; DB 8; Length 1899;  
Best Local Similarity 95.2%; Pred. No. 84;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GCAAGTCTGTAGTGGCGGG 21  
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Db 483 GCAAGTCTGTAGTGGCGGG 503

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RESULT 34
HUM8DC6Z/c
LOCUS
DEFINITION Homo sapiens (subclone H8 4_b9 from P1 35 H5 C8) DNA linear PRI 22-AUG-1994
ACCESSION L35661.1 GI:532026
VERSION MX1 region.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 3339)
Martin,C.H., Bondoc,M.M., Chiang,A., Cloutier,T., Davis,C.A.,
Ericsson,C.L., Jaklevic,M.A., Kim,R.J., Lee,M.T., Li,M.,
Mayeda,C.A., Steiert-Bl,Keir,A. and Palazzolo,M.J.
Sequencing of the MX1 region on human chromosome 21
Unpublished (1994)
ORIGINAL SOURCE text: Homo sapiens (library: Subclones in pSP72
from P1 clone 35 H5 C8 (H8)) DNA.
Sequence submitted by:
Human Genome Center and
Drosophila Genome Center
Lawrence Berkeley Laboratory
Berkeley, CA 94720
e-mail: seq@genome.lbl.gov
This subclone overlaps H8 6_e2 and H8 3_d9.
FEATURES
source
1..3339
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
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(H8)"
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Query Match 92.4%; Score 19.4; DB 8; Length 3339;
Best Local Similarity 95.2%; Pred. No. 84;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCTGTAGTGGCGGG 21
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Db 2664 GCAAGTCTGCAGTGGCGGG 2644
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RESULT 35
CS124352
LOCUS
DEFINITION Sequence 38 from Patent WO2005059172.
ACCESSION CS124352
VERSION CS124352.1 GI:71057417
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
Foekens,J.
METHOD and nucleic acids for the improved treatment of breast cell
proliferative disorders
Patent: WO 2005059172-A 38 30-JUN-2005;
JOURNAL Epigenomics AG (DE)
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/db_xref="taxon:9606"
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Best Local Similarity 95.2%; Pred. No. 84;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 GCAAGTCTGTAGTGGCGGG 21
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Db 1557 GCAAGTGTCTGCAGTGGCGGG 1577
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RESULT 36
HS25D2
LOCUS
DEFINITION Homo sapiens chromosome 21 from cosmid LL21NC02-25D2 map
21q22.2,D21S349-MX1, complete sequence.
ACCESSION AL773576 AJ011929 AL442167
VERSION AL773576.1 GI:21538700
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
Ramser,J., Francis,F., Beck,A., Hennig,S., Klages,S., Borzym,K.,
Langer,I., Steffens,C., Hildmann,T., Dagand,E., Yaspo,M.,
Reinhardt,R. and Lehrach,H.
Unpublished
2 (bases 1 to 40100)
MPIMG.
Direct Submission
Submitted (01-OCT-1998) MPIMG, Abt. Lehrach, Max Planck Institut
fuer Molekulare Genetik, Ihnestrasse 73, Berlin, 14195, Germany
Clones received from Resource Centre of the Human Genome Project at
the Max-Planck-Institut for Molecular Genetics.
This submission was part of AL442167 and AJ011929
Mapping info:
AL442166 1..300050
AL442167 1..313064
AL773569 (PAC RPCI-1 247E2)
AL773573 (PAC RPCI-1 146B4)
AL773572 (PAC RPCI-1 141D16)
AL773575 (PAC RPCI-1 269A14)
AL773570 (cosmid LNLCL16 44C5)
AL773578 (PAC RPCI-1 265B9)
AL773574 (cosmid LNLCL16 16H18)
AL773577 (cosmid LNLCL16 14C10)
AL773576 (cosmid LNLCL16 25D2)
AL773571 (cosmid LNLCL16 87D5)
AJ011929 592889..594336, cosmid LNLCL16 87DS 22828..24275 sequence
from clone KB447A5, accession no. AP001609 (DDBJ), sequenced at
KEIO university, Tokyo, Japan.
FEATURES
source
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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="21"
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/clone="LL21NC02-25D2"
/library, Lawrence Livermore National Laboratory (LLNL),
creator: Pieter de Jong; PAC: RPCI1,3-5, Roswell Park
Cancer Institute, creator: Pieter de Jong, P.Ioannou"
ORIGIN
Query Match 92.4%; Score 19.4; DB 8; Length 40100;
Best Local Similarity 95.2%; Pred. No. 86;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCTGTAGTGGCGGG 21
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Db 6042 GCAAGTGTCTGCAGTGGCGGG 6062
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RESULT 37
HS14C10
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LOCUS HS14C10 41120 bp DNA linear PRI 06-MAY-2003  
DEFINITION Homo sapiens chromosome 21 from cosmid LL21NC02-14C10 map  
ACCESSION 21q22.2,D21S349-MX1, complete sequence.  
VERSION AL773577 AJ011929 AL442167  
KEYWORDS HTG. AL773577.1 GI:21538704  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 Ramser,J., Francis,F., Beck,A., Hennig,S., Klages,S., Borzym,K.,  
AUTHORS Langer,I., Steffens,C., Hildmann,T., Dagand,E., Yaspo,M.,  
Reinhardt,R. and Lehrach,H.  
Unpublished  
2 (bases 1 to 41120)  
MPING.  
Direct Submission  
JOURNAL Submitted (01-OCT-1998) MPING, Abt. Lehrach, Max Planck Institut  
AUTHORS fuer Molekulare Genetik, Innestrasse 73, Berlin, 14195, Germany  
JOURNAL Clones received from Resource Centre of the Human Genome Project at  
TITLE the Max-Planck-Institut for Molecular Genetics  
COMMENT This submission was part of AL442167 and AJ011929  
Mapping info:  
AL442166 1..300050 <=> AJ011929 1..300050  
AL442167 1..313064 <=> AJ011929 300000..613064  
AL773569 (PAC RPCI-1 247E2) <=> AJ011929 1..153758  
AL773573 (PAC RPCI-1 146B4) <=> AJ011929 138212..246050  
AL773572 (PAC RPCI-1 14D16) <=> AJ011929 211573..357649  
AL773575 (PAC RPCI-1 269A14) <=> AJ011929 296228..392080  
AL773570 (cosmid LLNLC116 44C5) <=> AJ011929 362796..408363  
AL773578 (PAC RPCI-1 265B9) <=> AJ011929 384408..542081  
AL773574 (cosmid LLNLC116 16H18) <=> AJ011929 439926..475647  
AL773577 (cosmid LLNLC116 14C10) <=> AJ011929 514758..555921  
AL773576 (cosmid LLNLC116 25D2) <=> AJ011929 538954..579053  
AL773571 (cosmid LLNLC116 87D5) <=> AJ011929 570062..613064  
AJ011929 592889..594336, cosmid LLNLC116 87D5 22828..24275 sequence  
from clone KB447A5, accession no. AP001609 (DDBJ), sequenced at  
KEIO university, Tokyo, Japan.

FEATURES  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/chromosomes="21"  
/map="21q22.2,D21S349-MX1"  
/clone="LL21NC02-14C10"  
library, Lawrence Livermore National Laboratory (LLNL),  
creator: Pieter de Jong; PAC: RPCI1,3-5, Roswell Park  
Cancer Institute, creator: Pieter de Jong, P.Ioannou"

ORIGIN  
Query Match 92.4%; Score 19.4; DB 8; Length 41120;  
Best Local Similarity 95.2%; Pred. No. 86;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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Db 30194 GCAAGTGTCTGAGTGGCGGG 30214  
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RESULT 38  
AC005612 60904 bp DNA linear PRI 04-SEP-1998  
LOCUS Homo sapiens chromosome 21, p1 clone LBL#8 (LEBL H8), complete  
DEFINITION sequence.  
ACCESSION AC005612  
VERSION AC005612.1 GI:3540153  
KEYWORDS HTG.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominoidea; Homo.  
REFERENCE 1 (bases 1 to 60904)  
AUTHORS Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M.,  
Kadner,K., Miguel,T., Miller,C., Pitluck,S., Pollard,M.,  
Rojeski,H., Subramanian,S. and Martin,C.H.  
Sequencing of human chromosome 21  
Unpublished  
2 (bases 1 to 60904)  
AUTHORS Ricke,D.O.  
TITLE Large Scale Sequence Analysis and Annotation with the Sequence  
JOURNAL Comparison Analysis (SCAN) System  
REFERENCE 3 (bases 1 to 60904)  
AUTHORS Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M.,  
Davis,C.A., Kadner,K., Miguel,T., Pitluck,S., Pollard,M.,  
Rojeski,H., Subramanian,S. and Martin,C.H.  
Direct Submission  
JOURNAL Submitted (04-SEP-1998) Human Genome Center, DOE Joint Genome  
Institute, Lawrence Berkeley National Laboratory, MS 74-157,  
Berkeley, CA 94720, U.S.A.  
COMMENT Sequence submitted by:  
DOE Joint Genome Institute.

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/mol\_type="genomic DNA"  
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/notes="LEBL H8"  
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repeat\_region 423..565  
/rpt\_family="L1"  
repeat\_region 815..4661  
/rpt\_family="L1"  
repeat\_region 4917..4940  
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repeat\_region complement(6688..6819)  
/rpt\_family="Alu"  
repeat\_region 7441..7741  
/rpt\_family="Alu"  
repeat\_region 7724..7743  
/notes="(A)20"  
/rpt\_type=tandem  
/rpt\_unit="a"  
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/rpt\_family="MERS"  
repeat\_region complement(8811..9778)  
/rpt\_family="LTR5"  
repeat\_region complement(9970..10409)  
/rpt\_family="MER41"  
repeat\_region complement(11266..11344)  
/rpt\_family="LTR12"  
repeat\_region 12169..12204  
/notes="(GT)18"  
/rpt\_type=tandem  
/rpt\_unit="gt"  
repeat\_region complement(13074..13520)  
/rpt\_family="LTR7"  
repeat\_region complement(13974..14029)  
/rpt\_family="MERS"  
repeat\_region 15399..15473  
/rpt\_family="L1"  
misc\_feature 15697..15808  
/notes="GAIL 2 excellent exon, frame 0"

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repeat_region      complement(15858. .16136)
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repeat_region      17631. .17863
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repeat_region      complement(18991. .19253)
repeat_region      /rpt family="Alu"
repeat_region      complement(19424. .19715)
repeat_region      /rpt family="Alu"
misc_feature       20241. .20286
repeat_region      /note="GRAIL 2 excellent exon, frame 0"
repeat_region      21081. .21263
repeat_region      /rpt family="MER5"
repeat_region      21861. .22013
repeat_region      /rpt family="MER20"
repeat_region      complement(23391. .23728)
repeat_region      /rpt family="THE1"
misc_feature       23779. .23994
repeat_region      /note="GRAIL 2 excellent exon, frame 0"
repeat_region      complement(24012. .24087)
repeat_region      /rpt family="MLT1"
misc_feature       24957. .25094
repeat_region      /note="GRAIL 2 excellent exon, frame 1"
repeat_region      25319. .25585
repeat_region      /rpt family="Alu"
misc_feature       27635. .27825
repeat_region      /note="GRAIL 2 excellent exon, frame 0"
repeat_region      28141. .28430
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misc_feature       28834. .28966
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repeat_region      /note=" (T)24"
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repeat_region      /rpt_unit="t"
repeat_region      complement(32303. .32508)
repeat_region      /rpt family="Alu"
misc_feature       33424. .33584
repeat_region      /note="GRAIL 2 excellent exon, frame 0"
misc_feature       33976. .34117
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repeat_region      complement(34362. .34558)
repeat_region      /rpt family="Tigger1"
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repeat_region      complement(35034. .35111)
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repeat_region      complement(35713. .36022)
repeat_region      /rpt family="Alu"
repeat_region      36501. .36803
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repeat_region      36909. .36950
repeat_region      /note=" (GT)21"
repeat_region      /rpt_type=tandem
repeat_region      /rpt_unit="gt"
misc_feature       37127. .37266
repeat_region      /note="GRAIL 2 excellent exon, frame 2"
repeat_region      39543. .39822
repeat_region      /rpt family="Alu"
misc_feature       40592. .40840
repeat_region      /note="GRAIL 2 excellent exon, frame 1"
repeat_region      complement(40971. .41337)

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/rpt family="MER4"
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/rpt family="Alu"
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/rpt family="Alu"
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/rpt family="MSTAR"
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/rpt family="Alu"
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/note="GRAIL 2 excellent exon, frame 1"

ORIGIN
Query Match      92.4%; Score 19.4; DB 8; Length 60904;
Best Local Similarity 95.2%; Pred.No. 86;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  GCAAGTGTCTAGTGTGGGG 21
        |||||
Db      14035  GCAAGTGTCTAGTGTGGGG 14055

RESULT 39
AP001609
LOCUS      Homo sapiens genomic DNA, chromosome 21, clone:KB447A5, MX1-D21S171
DEFINITION region, complete sequence.
ACCESSION  AP001609
VERSION     AP001609.1 GI:7670563
KEYWORDS   HIT.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE  1 (bases 1 to 108927)
            Shimizu.N., Kudoh.J. and Shibuya.K.
            Homo sapiens genomic DNA, chromosome 21, clone:KB447A5, MX1-D21S171
            region
JOURNAL    Published Only in DataBase (2000)
REFERENCE  2 (bases 1 to 108927)
            Shimizu.N., Kudoh.J. and Shibuya.K.
            Direct Submission
            Submitted (04-APR-2000) Nobuyoshi Shimizu, Keio University, School
            of Medicine, Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo
            160-8582, Japan (E-mail:nshimizu@med.keio.ac.jp,
            Tel:81-3-3351-2370, Fax:81-3-3351-2370)

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FEATURES
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    /db_xref="taxon:9606"
    /chromosome="21"
    /clone="KB447AS"
    /cell_line="FLEB14-14"
    /cell_type="pre-pro-B cell"
    /clone_lib="Keio BAC library"

ORIGIN
  Query Match      92.4%; Score 19.4; DB 8; Length 108927;
  Best Local Similarity 95.2%; Pred. No. 86;
  Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCCTGTAGGTGCGGGG 21
      |||||
Db 28636 GCAAGTCCTGACAGTGGGGG 28656

RESULT 40
AC023611/c
LOCUS      221285 bp      DNA      linear      HTC 29-JUN-2000
DEFINITION Mus musculus clone CT7-9K21, WORKING DRAFT SEQUENCE, 62 unordered
            pieces.
ACCESSION AC023611
VERSION   AC023611.2 GI:8810277
KEYWORDS  HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE    Mus musculus (house mouse)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 221285)
AUTHORS   DOE Joint Genome Institute.
TITLE      Sequencing of Mouse
JOURNAL    Unpublished
REFERENCE 2 (bases 1 to 221285)
AUTHORS   DOE Joint Genome Institute.
TITLE      Direct Submission
JOURNAL    Submitted (16-FEB-2000) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
            On Jun 29, 2000 this sequence version replaced gi:6980221.
            -----Genome Center
            Center: Joint Genome Institute
            Center Code: JGI
            Web site: http://www.jgi.doe.gov
            -----
Project Information
Center Project Name: 956898
Center clone name: RG-MBAC_9K21
            -----
Summary Statistics
Consensus quality: 172196 bases at least Q40
Consensus quality: 196011 bases at least Q30
Consensus quality: 201702 bases at least Q20
Estimated insert size: 160000; pulse field gel estimation
Estimated insert size: 215185; sum-of-contigs estimation
Quality coverage: 6.26 in Q20 bases; pulse field gel estimation
Quality coverage: 4.65 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 62 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
            1 1033: contig of 1033 bp in length
            * 1034 1133: gap of unknown length
            * 1134 2542: contig of 1409 bp in length
            * 2543 2642: gap of unknown length
            *
            2643 3698: contig of 1056 bp in length
            * 3699 3798: gap of unknown length
            * 3799 4993: contig of 1195 bp in length
            * 4994 5093: gap of unknown length
            * 5094 6427: contig of 1334 bp in length
            * 6428 6527: gap of unknown length
            * 6528 7763: contig of 1236 bp in length
            * 7764 7864: gap of unknown length
            * 7864 8877: contig of 1014 bp in length
            * 8878 10256: contig of 1279 bp in length
            * 8878 10256: contig of 1279 bp in length
            * 10257 10356: gap of unknown length
            * 10357 11357: contig of 1000 bp in length
            * 11357 11456: gap of unknown length
            * 11457 12470: contig of 1014 bp in length
            * 12471 12570: gap of unknown length
            * 12571 13861: contig of 1291 bp in length
            * 13862 13961: gap of unknown length
            * 13962 15060: contig of 1099 bp in length
            * 15061 15161: gap of unknown length
            * 15161 16252: contig of 1092 bp in length
            * 16253 16352: gap of unknown length
            * 16353 17470: contig of 1118 bp in length
            * 17471 17570: gap of unknown length
            * 17571 18937: contig of 1267 bp in length
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            * 18938 20246: contig of 1309 bp in length
            * 20247 20346: gap of unknown length
            * 20347 21515: contig of 1169 bp in length
            * 21516 21615: gap of unknown length
            * 21616 22752: contig of 1137 bp in length
            * 22753 22852: gap of unknown length
            * 22853 24438: contig of 1586 bp in length
            * 24439 24539: gap of unknown length
            * 24539 25615: contig of 1077 bp in length
            * 25616 25715: gap of unknown length
            * 25716 26918: contig of 1203 bp in length
            * 26919 27018: gap of unknown length
            * 27019 28161: contig of 1143 bp in length
            * 28162 28261: gap of unknown length
            * 28262 29906: contig of 1645 bp in length
            * 29907 30006: gap of unknown length
            * 30007 31335: contig of 1329 bp in length
            * 31336 31435: gap of unknown length
            * 31436 32661: contig of 1226 bp in length
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            * 32762 34093: contig of 1332 bp in length
            * 34094 34193: gap of unknown length
            * 34194 35482: contig of 1289 bp in length
            * 35483 35582: gap of unknown length
            * 35583 37001: contig of 1419 bp in length
            * 37002 37101: gap of unknown length
            * 37102 38337: contig of 1236 bp in length
            * 38338 38437: gap of unknown length
            * 38438 39825: contig of 1388 bp in length
            * 39826 39925: gap of unknown length
            * 39926 41162: contig of 1237 bp in length
            * 41163 41262: gap of unknown length
            * 41263 42872: contig of 1610 bp in length
            * 42873 42972: gap of unknown length
            * 42973 44118: contig of 1146 bp in length
            * 44119 44218: gap of unknown length
            * 44219 45913: contig of 1695 bp in length
            * 45914 46013: gap of unknown length
            * 46014 47295: contig of 1282 bp in length
            * 47296 47395: gap of unknown length
            * 47396 48500: contig of 1105 bp in length
            * 48501 48600: gap of unknown length
            * 48601 50670: contig of 2070 bp in length
            * 50671 50770: gap of unknown length
            * 50771 52744: contig of 1974 bp in length
            * 52745 52844: gap of unknown length
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* 54281 54380: gap of unknown length
* 54381 56311: contig of 1931 bp in length
* 56312 56411: gap of unknown length
* 56412 59166: contig of 2755 bp in length
* 59167 59266: gap of unknown length
* 59267 62681: contig of 3415 bp in length
* 62682 62781: gap of unknown length
* 62782 65691: contig of 2910 bp in length
* 65692 65791: gap of unknown length
* 65792 69358: contig of 3567 bp in length
* 69359 69458: gap of unknown length
* 69459 71957: contig of 2499 bp in length
* 71958 72057: gap of unknown length
* 72058 76352: contig of 4295 bp in length
* 76353 76453: gap of unknown length
* 76453 79737: contig of 3285 bp in length
* 79738 79837: gap of unknown length
* 79838 86357: contig of 6520 bp in length
* 86358 86457: gap of unknown length
* 86458 90914: contig of 4457 bp in length
* 90915 91014: gap of unknown length
* 91015 96832: contig of 5818 bp in length
* 96833 96932: gap of unknown length
* 96933 103782: contig of 6850 bp in length
* 103783 103882: gap of unknown length
* 103883 110628: contig of 6746 bp in length
* 110629 110728: gap of unknown length
* 110729 116501: contig of 5773 bp in length
* 116502 116601: gap of unknown length
* 116602 123034: contig of 6433 bp in length
* 123035 123134: gap of unknown length
* 123135 130209: contig of 7075 bp in length
* 130210 130309: gap of unknown length
* 130310 141462: contig of 11153 bp in length
* 141463 141562: gap of unknown length
* 141563 149389: contig of 7827 bp in length
* 149390 149489: gap of unknown length
* 149490 157306: contig of 7817 bp in length
* 157307 157406: gap of unknown length
* 157407 167404: contig of 9998 bp in length
* 167405 167504: gap of unknown length
* 167505 185812: contig of 18308 bp in length
* 185813 185912: gap of unknown length
* 185913 205026: contig of 19114 bp in length
* 205027 205126: gap of unknown length
* 205127 221285: contig of 16159 bp in length.
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    2543..2642
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    3699..3798
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    4994..5093
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    6428..6527
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    8878..8977
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15061..15160
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Query Match
Best Local Similarity 92.4%; Score 19.4; DB 14; Length 221285;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGTGTAGGTGCGGG 21
Db 11528 GCAAGTGTGAAGTGTGCGGG 11508

RESULT 41
HS21C085 340000 bp DNA linear PRI 16-APR-2005
LOCUS Homo sapiens chromosome 21 segment HS21C085.
DEFINITION AL163285 AF001740 BA000005
ACCESSION AL163285.2 GI:7171384
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
    Hominoidea; Homo
REFERENCE
    1 (bases 1 to 340000)
    Hattori,M., Fujiyama,A., Taylor,T.D., Watanabe,H., Yada,T.,
    Park,H.S., Toyoda,A., Ishii,K., Totoki,Y., Choi,D.K., Soeda,E.,
    Ohki,M., Takagi,T., Sakaki,Y., Taudien,S., Blechschmidt,K.,
    Polley,A., Menzel,U., Delabar,J., Kumpf,K., Lehmann,R.,
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    Hennig,S., Riesselmann,L., Dagan,E., Wehrmeyer,S., Borzym,K.,
    Gardiner,K., Nizetic,D., Francis,F., Lehrach,H., Reinhardt,R. and
    Yaspo,M.L.
    Direct Submission
    Submitted (05-MAY-2000) The Chromosome 21 Mapping and Sequencing
    Consortium: * RIKEN Genomic Sciences Center, Human Genome Research
    Group * Institute of Molecular Biotechnology, Genome Analysis *
    Keio University School of Medicine, Dept. of Molecular Biology *
    GBF, Dept. of Genome Analysis * Max-Planck Institute for Molecular
    Genetics (addresses see below)
    The Chromosome 21 Mapping and Sequencing Consortium consists of
    * RIKEN Genomic Sciences Center, Human Genome Research Group, *
    Sagami-hara 228-8555, Japan,
    * e.mail: sakaki@gs.riken.go.jp
    * URL: http://hgp.gs.riken.go.jp/
    and
    * Institute of Molecular Biotechnology, Genome Analysis, *
    Beutenbergstrasse 11, D-07745 Jena, Germany,
    * e.mail: gscj-submit@genome.imb-jena.de
    * URL: http://genome.imb-jena.de/
    and
    * Keio University School of Medicine, Dept. of Molecular Biology, *
    Tokyo 160-8582, Japan,
    * e.mail: shimizu@mb-med.keio.ac.jp
    * URL: http://adenine.dmb.med.keio.ac.jp/
    and
    * GBF, Dept. of Genome Analysis,
    * Mascheroder Weg 1, D-38124 Braunschweig, Germany, * e.mail:
    info.genome@gbf.de
    * URL: http://genome.gbf.de/
    and
    * Max-Planck Institute for Molecular Genetics,
    * Ihnestrasse 73, D-14195 Berlin, Germany,
    * e.mail: info-chr21@molgen.mpg.de
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    Location/Qualifiers

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 DEFINITION  
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ACCESSION  
 CR450734  
 VERSION  
 HTG.  
 SOURCE  
 Danio rerio (zebrafish)  
 ORGANISM  
 Danio rerio  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

REFERENCE  
 1 (bases 1 to 69893)  
 Johnson, C.  
 Direct Submission  
 Submitted (22-DEC-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk  
 zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk  
 On Dec 23, 2004 this sequence version replaced gi:56744163.

COMMENT  
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 Genome Center  
 Center: Wellcome Trust Sanger Institute  
 Center code: SC  
 Web site: http://www.sanger.ac.uk  
 Contact: zfish-help@sanger.ac.uk  
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at [http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted.

Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhiqiong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see [http://www.sanger.ac.uk/Projects/D\\_rerio/fishmask.shtml](http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml) DKEY-53N24 is from a Zebrafish BAC library  
 VECTOR: pIndigoBAC-5.

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 Location/Qualifiers  
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Best Local Similarity 95.0%; Pred. No. 2.8e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGCGGG 20  
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 Db 52563 GCAAGTGCTGTAGTGCTGG 52544

RESULT 43  
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 LOCUS  
 DEFINITION  
 Colobus guereza clone OLG\_57 olfactory receptor-like protein gene, partial sequence.

ACCESSION  
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 VERSION  
 AY448313.1 GI:38634341  
 SOURCE  
 Colobus guereza (guereza)  
 ORGANISM  
 Colobus guereza  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Cercopithecoidea; Colobinae; Colobus.

REFERENCE  
 1 (bases 1 to 667)  
 Gilad, Y., Wiebe, V., Przeworski, M., Lancet, D. and Paabo, S.  
 Loss of Olfactory Receptor Genes Coincides with the Acquisition of Full Trichromatic Vision in Primates  
 PLOS Biol. 2 (1), 0120-0125 (2004)

REFERENCE  
 2 (bases 1 to 667)  
 Gilad, Y., Wiebe, V., Przeworski, M., Lancet, D. and Paabo, S.  
 Direct Submission  
 Submitted (20-OCT-2003) Max Plank Institute for Evolutionary Anthropology, Deutscher Platz 6, Leipzig 04103, Germany  
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gene

ORIGIN

Query Match 84.8%; Score 17.8; DB 8; Length 667;  
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 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 Db 217 GCAGTGCTGTAGTGAGGGG 197

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 DEFINITION  
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ACCESSION  
 AY448570  
 VERSION  
 AY448570.1 GI:38634598  
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 SOURCE  
 Trachypithecus auratus (Javan langur)  
 ORGANISM  
 Trachypithecus auratus  
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REFERENCE  
 1 (bases 1 to 667)  
 Gilad, Y., Wiebe, V., Przeworski, M., Lancet, D. and Paabo, S.  
 Loss of Olfactory Receptor Genes Coincides with the Acquisition of Full Trichromatic Vision in Primates  
 PLOS Biol. 2 (1), 0120-0125 (2004)

REFERENCE  
 2 (bases 1 to 667)  
 Gilad, Y., Wiebe, V., Przeworski, M., Lancet, D. and Paabo, S.  
 Direct Submission



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	product.									
ACCESSION	AF076122									
VERSION	AF076122.1 GI:5531765									
KEYWORDS										
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ORGANISM	Scomberomorus maculatus									
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	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;									
	Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes;									
	Scombroidei; Scombridae; Scomberomorus.									
REFERENCE	1 (bases 1 to 1047)									
AUTHORS	Banford,H.M., Bermingham,E., Collette,B.B. and McCafferty,S.S.									
TITLE	Phylogenetic systematics of the Scomberomorus regalis (Teleostei:Scombridae) species group: molecules, morphology and biogeography of Spanish mackerels									
JOURNAL	Unpublished									
REFERENCE	2 (bases 1 to 1047)									
AUTHORS	Banford,H.M., Bermingham,E., Collette,B.B. and McCafferty,S.S.									
TITLE	Direct Submission									
JOURNAL	Submitted (02-JUL-1998) Naos Laboratories, Smithsonian Tropical Research Institute, Unit 0948, APO, AA 34002-0948, USA									
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ORIGIN										

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DEFINITION Scomberomorus regalis isolate STR13836-nd2 NADH dehydrogenase
            subunit 2 gene, complete cds; mitochondrial gene for mitochondrial
            product.
ACCESSION AF076124.1 GI:5531767
VERSION AF076124
KEYWORDS mitochondrial Scomberomorus regalis
SOURCE Scomberomorus regalis
ORGANISM Scomberomorus regalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
            Scombroidei; Scombridae; Scomberomorus.
REFERENCE 1 (bases 1 to 1047)
AUTHORS Banford,H.M., Bermingham,E., Collette,B.B. and McCafferty,S.S.
TITLE Phylogenetic systematics of the Scomberomorus regalis
         (Teleostei:Scombridae) species group: molecules, morphology and
         biogeography of Spanish mackerels
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1047)
AUTHORS Banford,H.M., Bermingham,E., Collette,B.B. and McCafferty,S.S.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-1998) Naos Laboratories, Smithsonian Tropical
         Research Institute, Unit 0948, APO, AA 34002-0948, USA
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ORIGIN
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    Best Local Similarity 90.5%; Pred. No. 5.6e+02;
    Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTGCTGTAGTGGGGG 21
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Db 728 GCAAGGGCTGTAAGTGGGGG 708

RESULT 48
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LOCUS Scomberomorus maculatus isolate STR15090-nd2 NADH dehydrogenase
DEFINITION subunit 2 gene, complete cds; mitochondrial gene for mitochondrial
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ACCESSION AF076125
VERSION AF076125.1 GI:5531768
KEYWORDS mitochondrial Scomberomorus maculatus
SOURCE Scomberomorus maculatus
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            Scombroidei; Scombridae; Scomberomorus.
REFERENCE 1 (bases 1 to 1047)
AUTHORS Banford,H.M., Bermingham,E., Collette,B.B. and McCafferty,S.S.
TITLE Phylogenetic systematics of the Scomberomorus regalis
         (Teleostei:Scombridae) species group: molecules, morphology and
         biogeography of Spanish mackerels
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1047)
AUTHORS Banford,H.M., Bermingham,E., Collette,B.B. and McCafferty,S.S.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-1998) Naos Laboratories, Smithsonian Tropical
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AUTHORS Banford,H.M., Bermingham,E., Collette,B.B. and McCafferty,S.S.
TITLE Phylogenetic systematics of the Scomberomorus regalis
         (Teleostei:Scombridae) species group: molecules, morphology and
         biogeography of Spanish mackerels
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1047)
AUTHORS Banford,H.M., Bermingham,E., Collette,B.B. and McCafferty,S.S.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-1998) Naos Laboratories, Smithsonian Tropical
         Research Institute, Unit 0948, APO, AA 34002-0948, USA
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    Query Match 84.8%; Score 17.8; DB 5; Length 1047;
    Best Local Similarity 90.5%; Pred. No. 5.6e+02;
    Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTGCTGTAGTGGGGG 21
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Db 728 GCAAGGGCTGTAAGTGGGGG 708

RESULT 49
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LOCUS Scomberomorus regalis isolate HB872-nd2 NADH dehydrogenase subunit
DEFINITION 2 gene, complete cds; mitochondrial gene for mitochondrial product.
ACCESSION AF076126
VERSION AF076126.1 GI:5531769
KEYWORDS mitochondrial Scomberomorus regalis
SOURCE Scomberomorus regalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
            Scombroidei; Scombridae; Scomberomorus.
REFERENCE 1 (bases 1 to 1047)
AUTHORS Banford,H.M., Bermingham,E., Collette,B.B. and McCafferty,S.S.
TITLE Phylogenetic systematics of the Scomberomorus regalis
         (Teleostei:Scombridae) species group: molecules, morphology and
         biogeography of Spanish mackerels
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1047)
AUTHORS Banford,H.M., Bermingham,E., Collette,B.B. and McCafferty,S.S.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-1998) Naos Laboratories, Smithsonian Tropical
         Research Institute, Unit 0948, APO, AA 34002-0948, USA
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LPLTPALTITLTL"

## ORIGIN

Query Match 84.8%; Score 17.8; DB 5; Length 1047;  
Best Local Similarity 90.5%; Pred. No. 5.6e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGGCGGG 21  
||||| ||||| ||||| |||||  
Db 728 GCAAGGGCTGTAAGTGGCGG 708

## RESULT 50

AF076127/c

## LOCUS

DEFINITION AF076127 1047 bp DNA linear VRT 20-JUL-1999  
Scomberomorus maculatus isolate HB261-nd2 NADH dehydrogenase  
subunit 2 gene, complete cds; mitochondrial gene for mitochondrial  
product.

## ACCESSION

AF076127

## VERSION

AF076127.1

## KEYWORDS

GI:5531770

## SOURCE

mitochondrion

## ORGANISM

Scomberomorus maculatus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Acanthomorpha; Acanthopterygii; Perciformes; Scombridae;  
Scombroidei; Scombridae; Scomberomorus.

1 (bases 1 to 1047)

Banford,H.M., Bermingham,E., Collette,B.B. and McCafferty,S.S.

Phylogenetic systematics of the Scomberomorus regalis

(Teleostei:Scombridae) species group: molecules, morphology and

biogeography of Spanish mackerels

Unpublished

2 (bases 1 to 1047)

Banford,H.M., Bermingham,E., Collette,B.B. and McCafferty,S.S.

Direct Submission

Submitted (02-JUL-1998) Naos Laboratories, Smithsonian Tropical

Research Institute, Unit 0948, APO, AA 34002-0948, USA

## FEATURES

Location/Qualifiers

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/mol\_type="genomic DNA"

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/db\_xref="GI:5531786"

/translation="MNPVILATLFLGLGTTTTFASSHWLLAWMGLENTLAIPLM

## ORIGIN

Query Match 84.8%; Score 17.8; DB 5; Length 1047;  
Best Local Similarity 90.5%; Pred. No. 5.6e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGGCGGG 21  
||||| ||||| ||||| |||||  
Db 728 GCAAGGGCTGTAAGTGGCGG 708

Search completed: January 27, 2006, 06:14:34  
Job time : 899 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 27, 2006, 04:45:58 ; Search time 72.5 Seconds  
(without alignments)  
514.880 Million cell updates/sec

Title: US-10-070-415A-37\_COPY\_410\_430

Perfect score: 21

Sequence: 1 gcaagtgtgttagtgctggggg 21

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents NA.\*

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- 9: /cgn2\_6/prodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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ALIGNMENTS

RESULT 1

US-09-813-031-1

Sequence 1, Application US/09813031

Patent No. 6667155

GENERAL INFORMATION:

APPLICANT: Hijikata, Minako

APPLICANT: Mishiro, Shunji

APPLICANT: Oota, Yasuhiko

APPLICANT: Hashimoto, Koji

TITLE OF INVENTION: CARRIER FOR GENE DETECTION AND ITS USE FOR DETECTING VALIDITY OF

TITLE OF INVENTION: INTERFERON THERAPY

FILE REFERENCE: 205058USOSRD

CURRENT APPLICATION NUMBER: US/09/813,031

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: JP2000-080955

PRIOR FILING DATE: 2000-03-22

PRIOR APPLICATION NUMBER: JP2001-062372

PRIOR FILING DATE: 2001-03-06

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1

LENGTH: 581

TYPE: DNA

ORGANISM: Homo sapiens

US-09-813-031-1

Query Match 92.4%; Score 19.4; DB 3; Length 581;

Best Local Similarity 95.2%; Pred. No. 7.5;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

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DB

( 410 GCAAGTCTGMAGTGGGGG 430

RESULT 2

US-09-813-031-2

Sequence 2, Application US/09813031

Patent No. 6667155

GENERAL INFORMATION:

APPLICANT: Hijikata, Minako

APPLICANT: Mishiro, Shunji

APPLICANT: Oota, Yasuhiko

APPLICANT: Hashimoto, Koji

TITLE OF INVENTION: CARRIER FOR GENE DETECTION AND ITS USE FOR DETECTING VALIDITY OF

TITLE OF INVENTION: INTERFERON THERAPY

FILE REFERENCE: 205058USOSRD

CURRENT APPLICATION NUMBER: US/09/813,031

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: JP2000-080955

PRIOR FILING DATE: 2000-03-22

PRIOR APPLICATION NUMBER: JP2001-062372

PRIOR FILING DATE: 2001-03-06

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn version 3.1

SEQ ID NO 2

LENGTH: 581

TYPE: DNA

ORGANISM: Homo sapiens

US-09-813-031-2

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Best Local Similarity 95.2%; Pred. No. 7.5;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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; Patent No. 6783935
; GENERAL INFORMATION:
; APPLICANT: HIJIKATA, MINAKO
; APPLICANT: MISHIRO, SHUNJI
; APPLICANT: OOTA, YASUHIKO
; APPLICANT: HASHIMOTO, KOJI
; TITLE OF INVENTION: GENETIC POLYMORPHISM OF MXA PROTEIN AND USE THEREOF
; FILE REFERENCE: 205057US0SRD
; CURRENT APPLICATION NUMBER: US/09/813,990A
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: JP2000-080955
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: JP2001-062371
; PRIOR FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-813-990A-1

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Best Local Similarity 95.2%; Pred. No. 7.5;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTGTCTGAGTGGCGGG 21
Db 410 GCAAGTGTCTGAGTGGCGGG 430

RESULT 6
US-09-813-990A-2
; Sequence 2, Application US/09813990A
; Patent No. 6783935
; GENERAL INFORMATION:
; APPLICANT: HIJIKATA, MINAKO
; APPLICANT: MISHIRO, SHUNJI
; APPLICANT: OOTA, YASUHIKO
; APPLICANT: HASHIMOTO, KOJI
; TITLE OF INVENTION: GENETIC POLYMORPHISM OF MXA PROTEIN AND USE THEREOF
; FILE REFERENCE: 205057US0SRD
; CURRENT APPLICATION NUMBER: US/09/813,990A
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: JP2000-080955
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: JP2001-062371
; PRIOR FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-813-990A-2

Query Match          92.4%; Score 19.4; DB 3; Length 581;
Best Local Similarity 95.2%; Pred. No. 7.5;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTGTCTGAGTGGCGGG 21
Db 410 GCAAGTGTCTGAGTGGCGGG 430

RESULT 7
US-09-813-990A-3
; Sequence 3, Application US/09813990A
; Patent No. 6783935
; GENERAL INFORMATION:
; APPLICANT: HIJIKATA, MINAKO
; APPLICANT: MISHIRO, SHUNJI
; APPLICANT: OOTA, YASUHIKO
; APPLICANT: HASHIMOTO, KOJI
; TITLE OF INVENTION: GENETIC POLYMORPHISM OF MXA PROTEIN AND USE THEREOF
; FILE REFERENCE: 205057US0SRD
; CURRENT APPLICATION NUMBER: US/09/813,990A
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: JP2000-080955
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: JP2001-062371
; PRIOR FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 23
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-813-990A-3

Query Match          92.4%; Score 19.4; DB 3; Length 581;
Best Local Similarity 95.2%; Pred. No. 7.5;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTGTCTGAGTGGCGGG 21
Db 410 GCAAGTGTCTGAGTGGCGGG 430

RESULT 8
US-09-813-990A-4
; Sequence 4, Application US/09813990A
; Patent No. 6783935
; GENERAL INFORMATION:
; APPLICANT: HIJIKATA, MINAKO
; APPLICANT: MISHIRO, SHUNJI
; APPLICANT: OOTA, YASUHIKO
; APPLICANT: HASHIMOTO, KOJI
; TITLE OF INVENTION: GENETIC POLYMORPHISM OF MXA PROTEIN AND USE THEREOF
; FILE REFERENCE: 205057US0SRD
; CURRENT APPLICATION NUMBER: US/09/813,990A
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: JP2000-080955
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: JP2001-062371
; PRIOR FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 581
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-813-990A-4

Query Match          92.4%; Score 19.4; DB 3; Length 581;
Best Local Similarity 95.2%; Pred. No. 7.5;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTGTCTGAGTGGCGGG 21
Db 410 GCAAGTGTCTGAGTGGCGGG 430

RESULT 9
US-09-949-016-805/c
; Sequence 805, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 805
; LENGTH: 3302
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-805
```

```
Query Match      81.0%; Score 17; DB 3; Length 3302;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      5 GTGCTGTAGTGCGGGG 21
          |||
Db      541 GTGCTGTAGTGCGGGG 525
```

```
RESULT 10
US-09-949-016-1888/c
; Sequence 1888, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1888
; LENGTH: 3304
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1888
```

```
Query Match      81.0%; Score 17; DB 3; Length 3304;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      5 GTGCTGTAGTGCGGGG 21
          |||
Db      542 GTGCTGTAGTGCGGGG 526
```

```
RESULT 11
US-09-949-016-12547/c
; Sequence 12547, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
```

```
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12547
; LENGTH: 49389
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12547
```

```
Query Match      81.0%; Score 17; DB 3; Length 49389;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      5 GTGCTGTAGTGCGGGG 21
          |||
Db      21458 GTGCTGTAGTGCGGGG 21442
```

```
RESULT 12
US-09-949-016-13630/c
; Sequence 13630, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13630
; LENGTH: 49389
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13630
```

```
Query Match      81.0%; Score 17; DB 3; Length 49389;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      5 GTGCTGTAGTGCGGGG 21
          |||
Db      21458 GTGCTGTAGTGCGGGG 21442
```

```
RESULT 13
US-09-857-524B-9/c
; Sequence 9, Application US/09857524B
; Patent No. 6864077
; GENERAL INFORMATION:
; APPLICANT: Edgar B. Cahoon
; APPLICANT: Rebecca E. Cahoon
; APPLICANT: William D. Hitz
; APPLICANT: Anthony J. Kinney
; TITLE OF INVENTION: Membrane-Bound Desaturases
; FILE REFERENCE: BB1264
; CURRENT APPLICATION NUMBER: US/09/857,524B
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/110,784
; PRIOR FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
```



```
/ LENGTH: 1972
/ TYPE: DNA
/ ORGANISM: Triticum aestivum
US-09-857-524B-9

Query Match      80.0%; Score 16.8; DB 3; Length 1972;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 20
   |||||
Db 829 GCAAGTGTCTAGGTGCGGG 810

RESULT 14
US-09-711-164-296/c
/ Sequence 296, Application US/09711164
/ Patent No. 6589738
/ GENERAL INFORMATION:
/ APPLICANT: Forsyth, R. Allyn
/ APPLICANT: Ohlsen, Kari
/ APPLICANT: Zyskind, Judith
/ TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERAPY
/ FILE REFERENCE: ELITRA.008A
/ CURRENT APPLICATION NUMBER: US/09/711,164
/ CURRENT FILING DATE: 2000-11-09
/ PRIOR APPLICATION NUMBER: US 60/164415
/ PRIOR FILING DATE: 1999-11-9
/ NUMBER OF SEQ ID NOS: 469
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 296
/ LENGTH: 4134
/ TYPE: DNA
/ ORGANISM: Escherichia coli
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)...(4134)
US-09-711-164-296

Query Match      80.0%; Score 16.8; DB 3; Length 4134;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 20
   |||||
Db 243 GTAAGTGTCTAGGTGCGGG 224

RESULT 15
US-09-453-702B-226/c
/ Sequence 226, Application US/09453702B
/ Patent No. 6365723
/ GENERAL INFORMATION:
/ APPLICANT: Blattner, Frederick R.
/ Burland, Valerie
/ Perna, Nicole T.
/ Plunkett, Guy
/ Welch, Rod
/ TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
/ NUMBER OF SEQUENCES: 265
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Quarles & Brady
/ STREET: 1 South Pinckney Street
/ CITY: Madison
/ STATE: WI
/ COUNTRY: US
/ ZIP: 53701-2113
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50 inch. 1.44mb storage
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Word Perfect 8.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/114,170
/ FILING DATE: 01-Apr-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/453,702
/ FILING DATE: 03-DEC-1999
/ APPLICATION NUMBER: 60/110,955
/ FILING DATE: 04-DEC-1998
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Seay, Nicholas J.
/ REGISTRATION NUMBER: 27386
/ REFERENCE/DOCKET NUMBER: 960296.95017
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (608) 251-5000
/ TELEFAX: (608) 251-9166
/ INFORMATION FOR SEQ ID NO: 226:
```

```
/ APPLICATION NUMBER: US/09/453,702B
/ FILING DATE: 03-Dec-1999
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/110,955
/ FILING DATE: 04-DEC-1998
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Seay, Nicholas J.
/ REGISTRATION NUMBER: 27386
/ REFERENCE/DOCKET NUMBER: 960296.95017
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (608) 251-5000
/ TELEFAX: (608) 251-9166
/ INFORMATION FOR SEQ ID NO: 226:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 5519
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ SEQUENCE DESCRIPTION: SEQ ID NO: 226:
US-09-453-702B-226

Query Match      80.0%; Score 16.8; DB 3; Length 5519;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 20
   |||||
Db 347 GTAAGTGTCTAGGTGCGGG 328

RESULT 16
US-10-114-170-226/c
/ Sequence 226, Application US/10114170
/ Patent No. 6855814
/ GENERAL INFORMATION:
/ APPLICANT: Blattner, Frederick R.
/ Burland, Valerie
/ Perna, Nicole T.
/ Plunkett, Guy
/ Welch, Rod
/ TITLE OF INVENTION: No. 6855814el Sequences of E. coli O157
/ NUMBER OF SEQUENCES: 265
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Quarles & Brady
/ STREET: 1 South Pinckney Street
/ CITY: Madison
/ STATE: WI
/ COUNTRY: US
/ ZIP: 53701-2113
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50 inch. 1.44mb storage
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Word Perfect 8.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/114,170
/ FILING DATE: 01-Apr-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/453,702
/ FILING DATE: 03-DEC-1999
/ APPLICATION NUMBER: 60/110,955
/ FILING DATE: 04-DEC-1998
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Seay, Nicholas J.
/ REGISTRATION NUMBER: 27386
/ REFERENCE/DOCKET NUMBER: 960296.95017
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (608) 251-5000
/ TELEFAX: (608) 251-9166
/ INFORMATION FOR SEQ ID NO: 226:
```

```

;
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 5519
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   SEQUENCE DESCRIPTION: SEQ ID NO: 226:
;
US-10-114-170-226

    Query Match      80.0%; Score 16.8; DB 3; Length 5519;
    Best Local Similarity 90.0%; Pred. No. 1.7e+02;
    Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  GCAAGTGCTGTAGTGC GGG 20
Db      347  GTAAGTGCTGTAGTGC GGG 328
          ||| ||||| ||||| |||||

RESULT 17
US-08-956-171E-45
; Sequence 45, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
;   APPLICANT: Charles Kunsch
;   Gil H. Choi
;   Patrick S. Dillon
;   Craig A. Rosen
;   Steven C. Barash
;   Michael R. Fannon
;   TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;   NUMBER OF SEQUENCES: 5256
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Human Genome Sciences, Inc.
;   STREET: 9410 Key West Avenue
;   CITY: Rockville
;   STATE: Maryland
;   COUNTRY: USA
;   ZIP: 20850
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;   COMPUTER: HP Vectra 486/33
;   OPERATING SYSTEM: MSDOS version 6.2
;   SOFTWARE: ASCII Text
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/956,171E
;   FILING DATE: 20-Oct-1997
;   CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 60/009,861
;   FILING DATE: January 5, 1996
;   APPLICATION NUMBER: 08/781,986
;   FILING DATE: January 3, 1997
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Mark J. Hyman
;   REGISTRATION NUMBER: 46,789
;   REFERENCE/DOCKET NUMBER: PB248P1
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (240) 314-1224
;   TELEFAX: (301) 309-8439
;   INFORMATION FOR SEQ ID NO: 45:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 9072 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   SEQUENCE DESCRIPTION: SEQ ID NO: 45:
;
US-08-956-171E-45

    Query Match      80.0%; Score 16.8; DB 3; Length 9072;
    Best Local Similarity 90.0%; Pred. No. 1.9e+02;
    Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  GCAAGTGCTGTAGTGC GGG 20

```

; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 188624  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-188624

Query Match 77.1%; Score 16.2; DB 3; Length 601;  
Best Local Similarity 85.7%; Pred. No. 2.5e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTCTGTAGTGGCGGG 21  
||||| ||||| ||||| |||||  
Db 40 GCAAGGGCTGTGGATCGGGG 60

RESULT 20  
US-09-949-016-188673  
; Sequence 188673, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 188673  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-188673

Query Match 77.1%; Score 16.2; DB 3; Length 601;  
Best Local Similarity 85.7%; Pred. No. 2.5e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTCTGTAGTGGCGGG 21  
||||| ||||| ||||| |||||  
Db 40 GCAAGGGCTGTGGATCGGGG 60

RESULT 21  
US-09-949-016-188722  
; Sequence 188722, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 188722  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human

US-09-949-016-188722

Query Match 77.1%; Score 16.2; DB 3; Length 601;  
Best Local Similarity 85.7%; Pred. No. 2.5e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTCTGTAGTGGCGGG 21  
||||| ||||| ||||| |||||  
Db 40 GCAAGGGCTGTGGATCGGGG 60

RESULT 22  
US-09-949-016-188771  
; Sequence 188771, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 188771  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-188771

Query Match 77.1%; Score 16.2; DB 3; Length 601;  
Best Local Similarity 85.7%; Pred. No. 2.5e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTCTGTAGTGGCGGG 21  
||||| ||||| ||||| |||||  
Db 40 GCAAGGGCTGTGGATCGGGG 60

RESULT 23  
US-09-949-016-192855  
; Sequence 192855, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 192855  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-192855

Query Match 77.1%; Score 16.2; DB 3; Length 601;  
Best Local Similarity 85.7%; Pred. No. 2.5e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGCGGG 21  
||||| ||||| |||||  
Db 40 GCAAGGGCTGTGGATGCGGG 60

## RESULT 24

US-09-949-016-192901  
; Sequence 192901, Application US/09949016  
; Patent No. 6812339

## GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 192901  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-192901

Query Match 77.1%; Score 16.2; DB 3; Length 601;  
Best Local Similarity 85.7%; Pred. No. 2.5e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGCGGG 21  
||||| ||||| |||||  
Db 40 GCAAGGGCTGTGGATGCGGG 60

## RESULT 25

US-09-949-016-192947  
; Sequence 192947, Application US/09949016  
; Patent No. 6812339

## GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 192947  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-192947

Query Match 77.1%; Score 16.2; DB 3; Length 601;  
Best Local Similarity 85.7%; Pred. No. 2.5e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGCGGG 21  
||||| ||||| |||||  
Db 40 GCAAGGGCTGTGGATGCGGG 60

## RESULT 26

US-09-949-016-192993  
; Sequence 192993, Application US/09949016  
; Patent No. 6812339

## GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 192993  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-192993

Query Match 77.1%; Score 16.2; DB 3; Length 601;  
Best Local Similarity 85.7%; Pred. No. 2.5e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGCGGG 21  
||||| ||||| |||||  
Db 40 GCAAGGGCTGTGGATGCGGG 60

## RESULT 27

US-09-949-016-193039  
; Sequence 193039, Application US/09949016  
; Patent No. 6812339

## GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 193039  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-193039

Query Match 77.1%; Score 16.2; DB 3; Length 601;  
Best Local Similarity 85.7%; Pred. No. 2.5e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGCGGG 21  
||||| ||||| |||||  
Db 40 GCAAGGGCTGTGGATGCGGG 60

## RESULT 28

US-09-949-016-193132  
; Sequence 193132, Application US/09949016  
; Patent No. 6812339

```
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 193132
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-193132

Query Match          77.1%; Score 16.2; DB 3; Length 601;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGGCGGG 21
Db 40 GCAAGGGCTGTGGATCGGGG 60

RESULT 29
US-09-949-016-193225
; Sequence 193225, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 193225
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-193225

Query Match          77.1%; Score 16.2; DB 3; Length 601;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGGCGGG 21
Db 40 GCAAGGGCTGTGGATCGGGG 60

RESULT 30
US-09-949-016-193318
; Sequence 193318, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
```

```
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 193318
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-193318

Query Match          77.1%; Score 16.2; DB 3; Length 601;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGGCGGG 21
Db 40 GCAAGGGCTGTGGATCGGGG 60

RESULT 31
US-09-016-434-1413/C
; Sequence 1413, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1413:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1282 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 9516319
US-09-016-434-1413
```

```

Query Match          77.1%; Score 16.2; DB 3; Length 1282;
Best Local Similarity 85.7%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  GCAAGTGTCTAGGTGCGGG 21
Db      572  GCGGGTCTAGGTAGGCGG 552

RESULT 32
US-09-949-016-17236
; Sequence 17236, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17236
; LENGTH: 48682
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17236

Query Match          77.1%; Score 16.2; DB 3; Length 48682;
Best Local Similarity 85.7%; Pred. No. 4.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  GCAAGTGTCTAGGTGCGGG 21
Db      5084  GCAAGGCTGTGGATGCGGG 5104

RESULT 33
US-09-949-016-17237
; Sequence 17237, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17237
; LENGTH: 48682
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17237

Query Match          77.1%; Score 16.2; DB 3; Length 48682;
Best Local Similarity 85.7%; Pred. No. 4.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  GCAAGTGTCTAGGTGCGGG 21

```

```

Db      5084  GCAAGGCTGTGGATGCGGG 5104

RESULT 34
US-09-949-016-17238
; Sequence 17238, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17238
; LENGTH: 48682
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17238

Query Match          77.1%; Score 16.2; DB 3; Length 48682;
Best Local Similarity 85.7%; Pred. No. 4.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  GCAAGTGTCTAGGTGCGGG 21
Db      5084  GCAAGGCTGTGGATGCGGG 5104

RESULT 35
US-09-949-016-17239
; Sequence 17239, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17239
; LENGTH: 48682
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17239

Query Match          77.1%; Score 16.2; DB 3; Length 48682;
Best Local Similarity 85.7%; Pred. No. 4.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  GCAAGTGTCTAGGTGCGGG 21
Db      5084  GCAAGGCTGTGGATGCGGG 5104

RESULT 36

```

```
US-09-949-016-17135
; Sequence 17135, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17135
; LENGTH: 51022
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17135

Query Match          77.1%; Score 16.2; DB 3; Length 51022;
Best Local Similarity 85.7%; Pred. No. 4.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGGCGGG 21
Db 5084 GCAAGGGCTGTGATCGGGG 5104

RESULT 37
US-09-949-016-17136
; Sequence 17136, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17136
; LENGTH: 51022
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17136

Query Match          77.1%; Score 16.2; DB 3; Length 51022;
Best Local Similarity 85.7%; Pred. No. 4.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGGCGGG 21
Db 5084 GCAAGGGCTGTGATCGGGG 5104

RESULT 38
US-09-949-016-17137
; Sequence 17137, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17137
; LENGTH: 51022
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17137

Query Match          77.1%; Score 16.2; DB 3; Length 51022;
Best Local Similarity 85.7%; Pred. No. 4.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGGCGGG 21
Db 5084 GCAAGGGCTGTGATCGGGG 5104

RESULT 39
US-09-949-016-17138
; Sequence 17138, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17138
; LENGTH: 51022
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17138

Query Match          77.1%; Score 16.2; DB 3; Length 51022;
Best Local Similarity 85.7%; Pred. No. 4.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGGCGGG 21
Db 5084 GCAAGGGCTGTGATCGGGG 5104

RESULT 40
US-09-949-016-17240
; Sequence 17240, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
```

Query Match	Best Local Similarity	Score	DB	Length	Indels	Mismatches	Gaps
<p>Prior Application Number: 60/241,755</p> <p>Prior Filing Date: 2000-10-20</p> <p>Prior Application Number: 60/237,768</p> <p>Prior Filing Date: 2000-10-03</p> <p>Prior Application Number: 60/231,498</p> <p>Prior Filing Date: 2000-09-08</p> <p>Number of Seq ID NOS: 207012</p> <p>Software: FastSeq for Windows Version 4.0</p> <p>Seq ID NO 17240</p> <p>Length: 86213</p> <p>Type: DNA</p> <p>Organism: Human</p> <p>US-09-949-016-17240</p>	77.1%	85.7%	16.2	86213	0	0	0
<p>Query Match</p> <p>Best Local Similarity</p> <p>Matches</p>	18	Conservative	0	Mismatches	3	Indels	0
<p>Qy 1 GCAAGTCTGTAGTGGGG 21</p> <p>     </p>	5084	GCAAGGCTGTGCATCGGG 5104					
<p>RESULT 41</p> <p>US-09-949-016-17241</p> <p>Sequence 17241, Application US/09949016</p> <p>Patent No. 6812339</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: VENTER, J. Craig et al.</p> <p>TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF</p> <p>TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF</p> <p>FILE REFERENCE: CL001307</p> <p>CURRENT APPLICATION NUMBER: US/09/949,016</p> <p>CURRENT FILING DATE: 2000-04-14</p> <p>Prior Application Number: 60/241,755</p> <p>Prior Filing Date: 2000-10-20</p> <p>Prior Application Number: 60/237,768</p> <p>Prior Filing Date: 2000-10-03</p> <p>Prior Application Number: 60/231,498</p> <p>Prior Filing Date: 2000-09-08</p> <p>Number of Seq ID NOS: 207012</p> <p>Software: FastSeq for Windows Version 4.0</p> <p>Seq ID NO 17241</p> <p>Length: 86213</p> <p>Type: DNA</p> <p>Organism: Human</p> <p>US-09-949-016-17241</p>	77.1%	85.7%	16.2	86213	0	0	0
<p>Query Match</p> <p>Best Local Similarity</p> <p>Matches</p>	18	Conservative	0	Mismatches	3	Indels	0
<p>Qy 1 GCAAGTCTGTAGTGGGG 21</p> <p>     </p>	5084	GCAAGGCTGTGCATCGGG 5104					
<p>RESULT 42</p> <p>US-09-949-016-17242</p> <p>Sequence 17242, Application US/09949016</p> <p>Patent No. 6812339</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: VENTER, J. Craig et al.</p> <p>TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF</p> <p>TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF</p> <p>FILE REFERENCE: CL001307</p> <p>CURRENT APPLICATION NUMBER: US/09/949,016</p> <p>CURRENT FILING DATE: 2000-04-14</p> <p>Prior Application Number: 60/241,755</p> <p>Prior Filing Date: 2000-10-20</p> <p>Prior Application Number: 60/237,768</p> <p>Prior Filing Date: 2000-10-03</p> <p>Prior Application Number: 60/231,498</p>	77.1%	85.7%	16.2	86213	0	0	0
<p>Query Match</p> <p>Best Local Similarity</p> <p>Matches</p>	18	Conservative	0	Mismatches	3	Indels	0
<p>Qy 1 GCAAGTCTGTAGTGGGG 21</p> <p>     </p>	5084	GCAAGGCTGTGCATCGGG 5104					





```
;
; FILING DATE: NO. 5753488ember 23, 1993
; APPLICATION NUMBER: 07/887,502
; FILING DATE: May 22, 1992
; APPLICATION NUMBER: 07/704,814
; FILING DATE: May 23, 1991
; APPLICATION NUMBER: 07/763,039
; FILING DATE: September 20, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 213/300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 545 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION:
;
US-08-465-388-43

Query Match 75.2%; Score 15.8; DB 2; Length 545;
Best Local Similarity 89.5%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAAGTGCTGTAGTGGCGG 20
Db 116 CAAGTGCTGAAGTGCGCG 98

RESULT 48
US-09-949-016-94093
; Sequence 94093, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94093
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-94093

Query Match 75.2%; Score 15.8; DB 3; Length 601;
Best Local Similarity 89.5%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGCGG 19
Db 154 GCAAGTGCTGTAGTGGCTG 172

RESULT 49
US-09-949-016-183284/c
; Sequence 183284, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94093
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-183284

Query Match 75.2%; Score 15.8; DB 3; Length 601;
Best Local Similarity 89.5%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AAGTGCTGTAGTGGCGGG 21
Db 419 AAGTGCTGTAGTGAAGGG 401

RESULT 50
US-08-840-683-2
; Sequence 2, Application US/08840683
; Patent No. 5821051
; GENERAL INFORMATION:
; APPLICANT: Androphy, Elliot J.
; APPLICANT: Chen, Jason J.
; TITLE OF INVENTION: B6-BINDING PROTEINS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/840,683
; FILING DATE: 29-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/273,059
; FILING DATE: 08-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: NEP-003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 688 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
;
US-08-840-683-2
```

Query Match 75.2%; Score 15.8; DB 2; Length 688;  
 Best Local Similarity 89.5%; Pred. No. 3.9e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 CAAGTGTGTAGTGGGG 20  
 |||||  
 Db 600 CAAGTGTGTAGTGGGG 618  
 |||||

Search completed: January 27, 2006, 07:08:54  
 Job time : 73.5 secs

**This Page Blank (uspto)**

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OM nucleic - nucleic search, using sw model

Run on: January 27, 2006, 05:44:44 ; Search time 396 Seconds  
(without alignments)  
44.051 Million cell updates/sec

Title: US-10-070-415A-37\_COPY\_410\_430

Perfect score: 21  
Sequence: 1 gcaagtgtgttagtgcgggg 21

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6059551 seqs, 415333918 residues

Total number of hits satisfying chosen parameters: 12119102

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Published Applications\_NA\_New.\*  
1: /cgn2\_6/prodata/2/pubpna/US08\_NEW\_PUB.seq.\*  
2: /cgn2\_6/prodata/2/pubpna/US06\_NEW\_PUB.seq.\*  
3: /cgn2\_6/prodata/2/pubpna/US07\_NEW\_PUB.seq.\*  
4: /cgn2\_6/prodata/2/pubpna/PCT\_NEW\_PUB.seq.\*  
5: /cgn2\_6/prodata/2/pubpna/US05\_NEW\_PUB.seq.\*  
6: /cgn2\_6/prodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
7: /cgn2\_6/prodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
8: /cgn2\_6/prodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
9: /cgn2\_6/prodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
10: /cgn2\_6/prodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
11: /cgn2\_6/prodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16.2	77.1	270	8	US-11-043-752-2597
2	16.2	77.1	1090	7	US-10-750-185-35695
3	16.2	77.1	1090	7	US-10-750-623-36139
4	16.2	77.1	42823	8	US-11-066-725-18
5	16.2	77.1	163162	8	US-11-121-086-66
6	15.4	73.3	21	7	US-10-310-914A-145269
7	15.4	72.4	25	8	US-11-136-527-306462
8	15.2	72.4	489	8	US-11-136-527-3610
9	15.2	72.4	489	8	US-11-136-527-7706
10	15.2	72.4	636	7	US-10-793-626-743
11	15.2	72.4	870	7	US-10-793-626-63
12	15.2	72.4	1400	8	US-11-136-527-6488
13	15.2	72.4	1635	6	US-10-978-927-4
14	15.2	72.4	1635	6	US-10-978-927-11
15	15.2	72.4	1671	7	US-10-821-234-657
16	15.2	72.4	1857	6	US-10-978-927-16
17	15.2	72.4	1857	7	US-10-947-249-196
18	15.2	72.4	2094	7	US-10-750-185-31951
19	15.2	72.4	2094	7	US-10-750-623-31951
20	15.2	72.4	3032	7	US-10-793-626-3924
21	15.2	72.4	3370	7	US-10-793-626-4190
22	15.2	72.4	3374	8	US-11-136-527-2392

C 23	15.2	72.4	4019	7	US-10-793-626-4210	Sequence 4210, Ap
C 24	15.2	72.4	4020	7	US-10-750-185-36139	Sequence 36139, A
C 25	15.2	72.4	4020	7	US-10-750-623-36139	Sequence 36139, A
C 26	15.2	72.4	4036	7	US-10-793-626-4287	Sequence 4287, Ap
C 27	15.2	72.4	11110	6	US-10-978-927-20	Sequence 20, Appl
C 28	15.2	72.4	12263	6	US-10-978-927-19	Sequence 19, Appl
C 29	15.2	72.4	23907	8	US-11-186-731-4	Sequence 4, Appl
C 30	15.2	72.4	24120	8	US-11-186-731-4	Sequence 6, Appl
C 31	15.2	72.4	175673	8	US-11-121-086-55	Sequence 55, Appl
C 32	15.2	72.4	285300	7	US-10-857-780-6	Sequence 6, Appl
C 33	15.2	72.4	1691140	8	US-11-091-018-1	Sequence 1, Appl
C 34	14.8	70.5	874	7	US-10-750-185-47833	Sequence 47833, A
C 35	14.8	70.5	874	7	US-10-750-623-47833	Sequence 47833, A
C 36	14.8	70.5	1187	7	US-10-750-185-46874	Sequence 46874, A
C 37	14.8	70.5	1187	7	US-10-750-623-46874	Sequence 46874, A
C 38	14.8	70.5	1258	7	US-10-750-185-46077	Sequence 46077, A
C 39	14.8	70.5	1258	7	US-10-750-623-46077	Sequence 46077, A
C 40	14.8	70.5	1321	7	US-10-750-185-63637	Sequence 63637, A
C 41	14.8	70.5	1321	7	US-10-750-623-63637	Sequence 63637, A
C 42	14.8	70.5	1444	8	US-11-000-680-138	Sequence 138, App
C 43	14.8	70.5	3331	7	US-10-750-185-41819	Sequence 41819, A
C 44	14.8	70.5	3331	7	US-10-750-623-41819	Sequence 41819, A
C 45	14.8	70.5	3404	7	US-10-750-185-52746	Sequence 52746, A
C 46	14.8	70.5	3404	7	US-10-750-623-52746	Sequence 52746, A
C 47	14.8	70.5	7142	7	US-10-516-768-22	Sequence 22, Appl
C 48	14.6	69.5	201	7	US-10-995-561-65200	Sequence 65200, A
C 49	14.6	69.5	201	7	US-10-995-561-82368	Sequence 82368, A
C 50	14.6	69.5	201	7	US-10-995-561-82380	Sequence 82380, A
C 51	14.6	69.5	600	8	US-11-136-527-7944	Sequence 7944, Ap
C 52	14.6	69.5	618	8	US-11-136-527-3948	Sequence 3948, Ap
C 53	14.6	69.5	975	7	US-10-750-185-41153	Sequence 41153, A
C 54	14.6	69.5	975	7	US-10-750-623-41153	Sequence 41153, A
C 55	14.6	69.5	1007	5	US-09-978-360A-377	Sequence 377, App
C 56	14.6	69.5	1103	7	US-10-750-185-41938	Sequence 41938, A
C 57	14.6	69.5	1103	7	US-10-750-623-41938	Sequence 41938, A
C 58	14.6	69.5	1160	7	US-10-750-185-26499	Sequence 26499, A
C 59	14.6	69.5	1160	7	US-10-750-623-26499	Sequence 26499, A
C 60	14.6	69.5	1243	7	US-10-750-185-63749	Sequence 63749, A
C 61	14.6	69.5	1243	7	US-10-750-623-63749	Sequence 63749, A
C 62	14.6	69.5	1277	7	US-10-750-185-53108	Sequence 53108, A
C 63	14.6	69.5	1277	7	US-10-750-623-53108	Sequence 53108, A
C 64	14.6	69.5	1291	7	US-10-750-185-62669	Sequence 62669, A
C 65	14.6	69.5	1291	7	US-10-750-623-62669	Sequence 62669, A
C 66	14.6	69.5	1329	7	US-10-750-185-34351	Sequence 34351, A
C 67	14.6	69.5	1329	7	US-10-750-623-34351	Sequence 34351, A
C 68	14.6	69.5	1335	7	US-10-750-185-27628	Sequence 27628, A
C 69	14.6	69.5	1335	7	US-10-750-623-27628	Sequence 27628, A
C 70	14.6	69.5	1382	7	US-10-750-185-42137	Sequence 42137, A
C 71	14.6	69.5	1382	7	US-10-750-623-42137	Sequence 42137, A
C 72	14.6	69.5	1558	7	US-10-750-185-42718	Sequence 42718, A
C 73	14.6	69.5	1558	7	US-10-750-623-42718	Sequence 42718, A
C 74	14.6	69.5	1605	7	US-10-750-185-53178	Sequence 53178, A
C 75	14.6	69.5	1605	7	US-10-750-623-53178	Sequence 53178, A
C 76	14.6	69.5	1795	7	US-10-750-185-56552	Sequence 56552, A
C 77	14.6	69.5	1795	7	US-10-750-623-56552	Sequence 56552, A
C 78	14.6	69.5	1974	7	US-10-750-185-27606	Sequence 27606, A
C 79	14.6	69.5	1974	7	US-10-750-623-27606	Sequence 27606, A
C 80	14.6	69.5	1976	7	US-10-750-185-63562	Sequence 63562, A
C 81	14.6	69.5	1976	7	US-10-750-623-63562	Sequence 63562, A
C 82	14.6	69.5	2122	7	US-10-821-234-131	Sequence 131, App
C 83	14.6	69.5	2438	7	US-10-750-185-53163	Sequence 53163, A
C 84	14.6	69.5	2438	7	US-10-750-623-53163	Sequence 53163, A
C 85	14.6	69.5	2793	7	US-10-775-169-228	Sequence 228, App
C 86	14.6	69.5	2849	7	US-10-131-826A-171	Sequence 171, App
C 87	14.6	69.5	3177	8	US-11-108-528-41	Sequence 41, Appl
C 88	14.6	69.5	4402	8	US-11-136-527-2389	Sequence 2389, Ap
C 89	14.6	69.5	26737	7	US-10-995-561-13496	Sequence 13496, A
C 90	14.6	69.5	35344	7	US-10-995-561-13307	Sequence 13307, A
C 91	14.6	69.5	66916	7	US-10-995-561-13374	Sequence 13374, A
C 92	14.6	69.5	96345	8	US-11-112-908-35	Sequence 35, Appl
C 93	14.6	69.5	100000	8	US-11-124-368A-2881	Sequence 2881, Ap
C 94	14.6	69.5	127340	8	US-11-112-908-35	Sequence 35, Appl
C 95	14.6	69.5	153376	8	US-11-121-086-5	Sequence 5, Appl

Sequence 3, Appli  
Sequence 1, Appli  
Sequence 181, App  
Sequence 183, App  
Sequence 185, App

c 96 14.6 69.5 168516 8 US-11-121-086-3  
c 97 14.6 69.5 1080000 7 US-10-928-446A-1  
c 98 14.6 69.5 1080000 7 US-10-928-446A-181  
c 99 14.6 69.5 1080000 7 US-10-928-446A-183  
c 100 14.6 69.5 1080000 7 US-10-928-446A-185

# ALIGNMENTS

RESULT 1  
US-11-043-752-2597  
; Sequence 2597, Application US/11043752  
; Publication No. US20060014165A1  
; GENERAL INFORMATION:  
; APPLICANT: Hakonarson, Hakon  
; APPLICANT: Gurney, Mark E.  
; APPLICANT: Halapi, Eva  
; TITLE OF INVENTION: METHODS OF DIAGNOSIS AND TREATMENT FOR  
; TITLE OF INVENTION: ASTHMA AND OTHER RESPIRATORY DISEASES BASED ON HAPLOTYPE  
; FILE REFERENCE: 2345.2044-003  
; CURRENT APPLICATION NUMBER: US/11/043,752  
; CURRENT FILING DATE: 2005-01-26  
; PRIOR APPLICATION NUMBER: PCT/US04/022446  
; PRIOR FILING DATE: 2004-07-14  
; PRIOR APPLICATION NUMBER: 60/487,072  
; PRIOR FILING DATE: 2003-07-14  
; PRIOR APPLICATION NUMBER: 60/559,611  
; PRIOR FILING DATE: 2004-04-05  
; NUMBER OF SEQ ID NOS: 4326  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2597  
; LENGTH: 270  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-043-752-2597

Query Match 77.1%; Score 16.2; DB 8; Length 270;  
Best Local Similarity 85.7%; Pred. No. 1.4e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAAGTCTGTAGTGGGG 21  
Db 242 GCAAGTCTGTGGAGCTGGG 262

RESULT 2  
US-10-750-185-35695/c  
; Sequence 35695, Application US/10750185  
; Publication No. US20050260603A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-2  
; CURRENT APPLICATION NUMBER: US/10/750,185  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 35695  
; LENGTH: 1090  
; TYPE: DNA  
; ORGANISM: Bovine 19866881301896  
US-10-750-185-35695

Query Match 77.1%; Score 16.2; DB 7; Length 1090;  
Best Local Similarity 85.7%; Pred. No. 1.6e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAAGTCTGTAGTGGGG 21  
Db 857 GCAGGTGCTGCGGTGCGGG 837

RESULT 3  
US-10-750-623-35695/c  
; Sequence 35695, Application US/10750623  
; Publication No. US20050287531A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-1  
; CURRENT APPLICATION NUMBER: US/10/750,623  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 35695  
; LENGTH: 1090  
; TYPE: DNA  
; ORGANISM: Bovine 19866881301896  
US-10-750-623-35695

Query Match 77.1%; Score 16.2; DB 7; Length 1090;  
Best Local Similarity 85.7%; Pred. No. 1.6e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAAGTCTGTAGTGGGG 21  
Db 857 GCAGGTGCTGCGGTGCGGG 837

RESULT 4  
US-11-066-725-18/c  
; Sequence 18, Application US/11066725  
; Publication No. US20050272680A1  
; GENERAL INFORMATION:  
; APPLICANT: Isis Pharmaceuticals Inc.  
; APPLICANT: Sanjay Bhanot  
; APPLICANT: Kenneth W. Dobie  
; APPLICANT: Xing-Xian Yu  
; APPLICANT: Brett P. Monia  
; TITLE OF INVENTION: MODULATION OF DIACYLGLYCEROL ACYLTRANSFERASE 2 EXPRESSION  
; FILE REFERENCE: RPS-0678US.C1  
; CURRENT APPLICATION NUMBER: US/11/066,725  
; CURRENT FILING DATE: 2005-02-24  
; PRIOR APPLICATION NUMBER: US/10/643,801  
; PRIOR FILING DATE: 2003-08-18  
; PRIOR APPLICATION NUMBER: PCT/US2004/024384  
; PRIOR FILING DATE: 2004-08-18  
; NUMBER OF SEQ ID NOS: 492  
; SEQ ID NO 18  
; LENGTH: 42823  
; TYPE: DNA  
; ORGANISM: H. sapiens  
; FEATURE:  
US-11-066-725-18

Query Match 77.1%; Score 16.2; DB 8; Length 42823;  
Best Local Similarity 85.7%; Pred. No. 2.3e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

100

US-11-136-527-7706

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Best Local Similarity 85.0%; Pred. No. 4.2e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGGG 20  
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Db 356 GCAAGAGCTGTCGGCGGG 375

RESULT 10

US-10-793-626-743  
; Sequence 743, Application US/10793626  
; Publication No. US20050255478A1  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: P03480US  
; CURRENT APPLICATION NUMBER: US/10793,626  
; CURRENT FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 743  
; LENGTH: 636  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: nucleic acid sequence  
US-10-793-626-743

Query Match 72.4%; Score 15.2; DB 7; Length 636;  
Best Local Similarity 85.0%; Pred. No. 4.4e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGGG 20  
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Db 457 GCAAGTTATGTAGTGCAGG 476

RESULT 11

US-10-793-626-63  
; Sequence 63, Application US/10793626  
; Publication No. US20050255478A1  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: P03480US  
; CURRENT APPLICATION NUMBER: US/10793,626  
; CURRENT FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 63  
; LENGTH: 870  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: nucleic acid sequence  
US-10-793-626-63

Query Match 72.4%; Score 15.2; DB 7; Length 870;  
Best Local Similarity 85.0%; Pred. No. 4.5e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGGG 20  
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Db 691 GCAAGTTATGTAGTGCAGG 710

RESULT 12

US-11-136-527-6488  
; Sequence 6488, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 6488  
; LENGTH: 1400  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-11-136-527-6488

Query Match 72.4%; Score 15.2; DB 8; Length 1400;  
Best Local Similarity 85.0%; Pred. No. 4.7e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGGG 20  
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Db 438 GCAAGGGCTGTAGTTCTGG 457

RESULT 13

US-10-978-927-4  
; Sequence 4, Application US/10978927  
; Publication No. US20060009406A1  
; GENERAL INFORMATION:  
; APPLICANT: Kyrkanides, Stephanos  
; TITLE OF INVENTION: VECTORS HAVING BOTH ISOFORMS OF  
; FILE REFERENCE: 21108.0018U2  
; CURRENT APPLICATION NUMBER: US/10/978,927  
; CURRENT FILING DATE: 2004-11-01  
; PRIOR APPLICATION NUMBER: PCT/US03/13672  
; PRIOR FILING DATE: 2003-05-02  
; PRIOR APPLICATION NUMBER: 60/377,503  
; PRIOR FILING DATE: 2002-05-02  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 1635  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Note =  
; OTHER INFORMATION: Synthetic Construct  
US-10-978-927-4

Query Match 72.4%; Score 15.2; DB 6; Length 1635;  
Best Local Similarity 85.0%; Pred. No. 4.8e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGGG 20  
||||| ||||| ||||| |||||

Db 1480 GCAAGTGCTGTGTGTGAGAG 1499

RESULT 14

US-10-978-927-11  
; Sequence 11, Application US/10978927  
; Publication No. US20060009406A1  
; GENERAL INFORMATION:  
; APPLICANT: Kyrkanides, Stephanos



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; TITLE OF INVENTION: VECTORS HAVING BOTH ISOFORMS OF
; FILE REFERENCE: BETA-HEXOSAMINIDASE
; FILE REFERENCE: 21108.0018U2
; CURRENT FILING DATE: 2004-11-01
; PRIOR APPLICATION NUMBER: US/10/978,927
; PRIOR FILING DATE: 2004-11-01
; PRIOR APPLICATION NUMBER: PCT/US03/13672
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 60/377,503
; PRIOR FILING DATE: 2002-05-02
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1635
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
; OTHER INFORMATION: Synthetic Construct
US-10-978-927-11

Query Match          72.4%; Score 15.2; DB 6; Length 1635;
Best Local Similarity 85.0%; Pred. No. 4.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GCAAGTGTCTGTAGTTCGGG 20
Db      1480 GCAAGTGTCTGTGGTGAGAG 1499

RESULT 15
US-10-821-234-657
; Sequence 657, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclapsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt SEQ_genes Version 1.0
; SEQ ID NO 657
; LENGTH: 1671
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-657

Query Match          72.4%; Score 15.2; DB 7; Length 1671;
Best Local Similarity 85.0%; Pred. No. 4.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GCAAGTGTCTGTAGTTCGGG 20
Db      1516 GCAAGTGTCTGTGGTGAGAG 1535

RESULT 16
US-10-978-927-16
; Sequence 16, Application US/10978927
; Publication No. US2006009406A1
; GENERAL INFORMATION:
; APPLICANT: Kyrkanides, Stephanos
; TITLE OF INVENTION: VECTORS HAVING BOTH ISOFORMS OF
; FILE OF INVENTION: BETA-HEXOSAMINIDASE
; FILE REFERENCE: 21108.0018U2
; CURRENT APPLICATION NUMBER: US/10/978,927
; CURRENT FILING DATE: 2004-11-01
; PRIOR APPLICATION NUMBER: PCT/US03/13672
```

```
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 60/377,503
; PRIOR FILING DATE: 2002-05-02
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1857
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
; OTHER INFORMATION: Synthetic Construct
US-10-978-927-16

Query Match          72.4%; Score 15.2; DB 6; Length 1857;
Best Local Similarity 85.0%; Pred. No. 4.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GCAAGTGTCTGTAGTTCGGG 20
Db      1591 GCAAGTGTCTGTGGTGAGAG 1610

RESULT 17
US-10-947-249-196
; Sequence 196, Application US/10947249
; Publication No. US20050287541A1
; GENERAL INFORMATION:
; APPLICANT: Akira NAKAGAWARA
; APPLICANT: Miki OHIRA
; APPLICANT: Shin ISHII
; APPLICANT: Takeshi GOTO
; APPLICANT: Hiroyuki KUBO
; APPLICANT: Takahiro HIRATA
; APPLICANT: Yasuko YOSHIDA
; APPLICANT: Saichi YAMADA
; TITLE OF INVENTION: Microarray for Predicting the Prognosis of Neuroblastoma and Me
; FILE OF INVENTION: Predicting the Prognosis of Neuroblastoma
; FILE REFERENCE: 117007
; CURRENT APPLICATION NUMBER: US/10/947,249
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US 60/505,614
; PRIOR APPLICATION NUMBER: 2003-09-25
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 196
; LENGTH: 1857
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-947-249-196

Query Match          72.4%; Score 15.2; DB 7; Length 1857;
Best Local Similarity 85.0%; Pred. No. 4.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GCAAGTGTCTGTAGTTCGGG 20
Db      1591 GCAAGTGTCTGTGGTGAGAG 1610

RESULT 18
US-10-750-185-31951/c
; Sequence 31951, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: Denise, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
```

```

; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31951
; LENGTH: 2094
; TYPE: DNA
; ORGANISM: Bovine 19866880495399
US-10-750-185-31951

Query Match          72.4%; Score 15.2; DB 7; Length 2094;
Best Local Similarity 85.0%; Pred. No. 4.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  GCAAGTGCTGTAGGTGCGG 20
DB      1613 GCAAGTGCTCCAGGTGAGG 1594

RESULT 19
US-10-750-623-31951/c
; Sequence 31951, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31951
; LENGTH: 2094
; TYPE: DNA
; ORGANISM: Bovine 19866880495399
US-10-750-623-31951

Query Match          72.4%; Score 15.2; DB 7; Length 2094;
Best Local Similarity 85.0%; Pred. No. 4.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  GCAAGTGCTGTAGGTGCGG 20
DB      1613 GCAAGTGCTCCAGGTGAGG 1594

RESULT 20
US-10-793-626-3924/c
; Sequence 3924, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3924
; LENGTH: 3032
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2392

Query Match          72.4%; Score 15.2; DB 8; Length 3374;
Best Local Similarity 85.0%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3924

Query Match          72.4%; Score 15.2; DB 7; Length 3032;
Best Local Similarity 85.0%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  GCAAGTGCTGTAGGTGCGG 20
DB      1352 GCAAGTTATGTAGGTGCAGG 1333

RESULT 21
US-10-793-626-4190
; Sequence 4190, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4190
; LENGTH: 3370
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-4190

Query Match          72.4%; Score 15.2; DB 7; Length 3370;
Best Local Similarity 85.0%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  GCAAGTGCTGTAGGTGCGG 20
DB      1288 GCAAGTTATGTAGGTGCAGG 1307

RESULT 22
US-11-136-527-2392
; Sequence 2392, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AMI01086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2392
; LENGTH: 3374
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2392

Query Match          72.4%; Score 15.2; DB 8; Length 3374;
Best Local Similarity 85.0%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

QY 1 GCAAGTGTCTAGGTGGG 20  
|||||  
Db 2412 GCAAGGCTGTAGGTCTGG 2431

## RESULT 23

US-10-793-626-4210/c  
; Sequence 4210, Application US/10793626  
; Publication No. US20050255478A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: MM1100-2  
; CURRENT APPLICATION NUMBER: US/10/793,626  
; CURRENT FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4210  
; LENGTH: 4019  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: nucleic acid sequence  
US-10-793-626-4210

Query Match 72.4%; Score 15.2; DB 7; Length 4019;  
Best Local Similarity 85.0%; Pred. No. 5.2e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGGG 20  
|||||  
Db 943 GCAAGTTATGTAGGTGAGG 924

## RESULT 24

US-10-750-185-36139/c  
; Sequence 36139, Application US/10750185  
; Publication No. US20050260603A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-2  
; CURRENT APPLICATION NUMBER: US/10/750,185  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 36139  
; LENGTH: 4020  
; TYPE: DNA  
; ORGANISM: Bovine 19866881456963  
US-10-750-185-36139

Query Match 72.4%; Score 15.2; DB 7; Length 4020;  
Best Local Similarity 85.0%; Pred. No. 5.2e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CAAGTGTCTAGGTGGG 21  
|||||  
Db 3278 CAAGTGTGAGGTGAGG 3259

## RESULT 25

US-10-750-623-36139/c

; Sequence 36139, Application US/10750623  
; Publication No. US20050287531A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-1  
; CURRENT APPLICATION NUMBER: US/10/750,623  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 36139  
; LENGTH: 4020  
; TYPE: DNA  
; ORGANISM: Bovine 19866881456963  
US-10-750-623-36139

Query Match 72.4%; Score 15.2; DB 7; Length 4020;  
Best Local Similarity 85.0%; Pred. No. 5.2e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CAAGTGTGTAGGTGGG 21  
|||||  
Db 3278 CAAGTGTGAGGTGAGG 3259

## RESULT 26

US-10-793-626-4287/c  
; Sequence 4287, Application US/10793626  
; Publication No. US20050255478A1  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/10/793,626  
; CURRENT FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4287  
; LENGTH: 4036  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: nucleic acid sequence  
US-10-793-626-4287

Query Match 72.4%; Score 15.2; DB 7; Length 4036;  
Best Local Similarity 85.0%; Pred. No. 5.2e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTGTGTAGGTGGG 20  
|||||  
Db 2681 GCAAGTTATGTAGGTGAGG 2662

## RESULT 27

US-10-978-927-20  
; Sequence 20, Application US/10978927  
; Publication No. US20060009406A1  
; GENERAL INFORMATION:  
; APPLICANT: Kyrkanides, Stephanos  
; TITLE OF INVENTION: VECTORS HAVING BOTH ISOFORMS OF

```

; TITLE OF INVENTION: BETA-HEXOSAMINIDASE
; FILE REFERENCE: 21108.001802
; CURRENT APPLICATION NUMBER: US/10/978,927
; CURRENT FILING DATE: 2004-11-01
; PRIOR APPLICATION NUMBER: PCT/US03/13672
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 60/377,503
; PRIOR FILING DATE: 2002-05-02
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 1110
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
; OTHER INFORMATION: Synthetic Construct
US-10-978-927-20

```

```

Query Match 72.4%; Score 15.2; DB 6; Length 1110;
Best Local Similarity 85.0%; Pred. No. 5.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 1 GCAAGTCTGTAGTGGGG 20
    ||||| ||||| ||||| |||||
DB 4060 GCAAGTCTGTGTGTGAGAG 4079

```

```

RESULT 28
US-10-978-927-19
; Sequence 19, Application US/10978927
; Publication No. US2006009406A1
; GENERAL INFORMATION:
; APPLICANT: Kytkanides, Stephanos
; TITLE OF INVENTION: VECTORS HAVING BOTH ISOFORMS OF
; FILE REFERENCE: 21108.001802
; CURRENT APPLICATION NUMBER: US/10/978,927
; CURRENT FILING DATE: 2004-11-01
; PRIOR APPLICATION NUMBER: PCT/US03/13672
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 60/377,503
; PRIOR FILING DATE: 2002-05-02
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 12263
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
; OTHER INFORMATION: Synthetic Construct
US-10-978-927-19

```

```

Query Match 72.4%; Score 15.2; DB 6; Length 12263;
Best Local Similarity 85.0%; Pred. No. 5.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 1 GCAAGTCTGTAGTGGGG 20
    ||||| ||||| ||||| |||||
DB 5213 GCAAGTCTGTGTGTGAGAG 5232

```

```

RESULT 29
US-11-186-731-6
; Sequence 6, Application US/11186731
; Publication No. US2005025521A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: 59079 and 12599, Protein Kinase Family
; TITLE OF INVENTION: Members and Uses Therefor
; FILE REFERENCE: MPI2001-047P1RCPl(M)

```

```

; CURRENT APPLICATION NUMBER: US/11/186,731
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/077,130
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/269201
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 23907
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-186-731-6

```

```

Query Match 72.4%; Score 15.2; DB 8; Length 23907;
Best Local Similarity 85.0%; Pred. No. 6.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 1 GCAAGTCTGTAGTGGGG 20
    ||||| ||||| ||||| |||||
DB 1017 GCAAGATCTGGAGTGGGG 1036

```

```

RESULT 30
US-11-186-731-4
; Sequence 4, Application US/11186731
; Publication No. US2005025521A1
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: 59079 and 12599, Protein Kinase Family
; TITLE OF INVENTION: Members and Uses Therefor
; FILE REFERENCE: MPI2001-047P1RCPl(M)
; CURRENT APPLICATION NUMBER: US/11/186,731
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/077,130
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/269201
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 24120
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)...(71)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (72)...(23978)
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: (23979)...(24120)
US-11-186-731-4

```

```

Query Match 72.4%; Score 15.2; DB 8; Length 24120;
Best Local Similarity 85.0%; Pred. No. 6.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 1 GCAAGTCTGTAGTGGGG 20
    ||||| ||||| ||||| |||||
DB 1088 GCAAGATCTGGAGTGGGG 1107

```

```

RESULT 31
US-11-121-086-55/c
; Sequence 55, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES

```

```
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 55
; LENGTH: 175673
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-55

Query Match      72.4%; Score 15.2; DB 8; Length 175673;
Best Local Similarity 85.0%; Pred. No. 7e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CAAGTCTCTAGTGGGGG 21
Db      128882 CAAGTCTCTGTGAGGGG 128863

RESULT 32
US-10-857-780-6/c
; Sequence 6, Application US/10857780
; Publication No. US20050272043A1
; GENERAL INFORMATION:
; APPLICANT: ROTH, RICHARD B.
; APPLICANT: BRAUN, ANDREAS
; APPLICANT: KAMMERER, STEFAN M.
; APPLICANT: NELSON, MATTHEW ROBERTS
; APPLICANT: RENELAND, RIKARD HENRY
; APPLICANT: HOYAL-WRIGHTSON, CAROLYN R.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: SEQ-4069-CP
; CURRENT APPLICATION NUMBER: US/10/857,780
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 10/723,681
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/490,234
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: 60/525,239
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 4962
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 285300
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3185)..(3185)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7922)..(7922)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10272)..(10272)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (28873)..(28873)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (29105)..(29106)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (35901)..(35901)
; OTHER INFORMATION: n is a, c, g, or t
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (36488)..(36488)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (40260)..(40260)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (52594)..(52594)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (68230)..(68230)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (70027)..(70027)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (83514)..(83514)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (89477)..(89477)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (108762)..(108762)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (109378)..(109378)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (113639)..(113639)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (115312)..(115312)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (115315)..(115315)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (127817)..(127817)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (138224)..(138224)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (140476)..(140476)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (147488)..(147488)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (147500)..(147500)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (147527)..(147527)
; OTHER INFORMATION: n is a, c, g, or t
```

```
;
;
; NAME/KEY: misc feature
; LOCATION: (147534)..(147534)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (171395)..(171395)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (195657)..(195657)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (196415)..(196415)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (196417)..(196417)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (212336)..(212337)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (212442)..(212442)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (212445)..(212445)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (212455)..(212455)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (215163)..(215163)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (217657)..(217657)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (217725)..(217725)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (231757)..(231757)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (231762)..(231762)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (235827)..(235827)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (241414)..(241414)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (248915)..(248915)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (250079)..(250079)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
```

```
;
; NAME/KEY: misc feature
; LOCATION: (250575)..(250575)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature

Query Match      72.4%; Score 15.2; DB 7; Length 285300;
Best Local Similarity 85.0%; Pred. No. 7e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2  CAAAGTCTGTAGGTGCGGG 21
      ||||| ||||| ||||| |||||
Db      255080  CAAACACTGTAGGTGCTGGG 255061

RESULT 33
US-11-091-018-1/c
; Sequence 1, Application US/11091018
; Publication No. US20050287551A1
; GENERAL INFORMATION:
; APPLICANT: Gretarsdottir, Solveig
; APPLICANT: Thorleifsson, Gudmar
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
; TITLE OF INVENTION: METHODS OF TREATMENT
; FILE REFERENCE: 2345.2010-016
; CURRENT APPLICATION NUMBER: US/11/091,018
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: PCT/US03/29906
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 10/255,120
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: 10/419,723
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 10/650,120
; PRIOR FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: 10/067,514
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 09/811,352
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1691140
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)....(1691140)
; OTHER INFORMATION: n=A,T,C or G
; US-11-091-018-1

Query Match      72.4%; Score 15.2; DB 8; Length 1691140;
Best Local Similarity 85.0%; Pred. No. 4.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  GCAAAGTCTGTAGGTGCGGG 20
      ||||| ||||| ||||| |||||
Db      421452  GCAAAGTGCAGGAGGTGCCGG 421433

RESULT 34
US-10-750-185-47833
; Sequence 47833, Application US/10750185
; Publication No. US200502603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
```

## ; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

; FILE REFERENCE: MM1100-2  
; CURRENT APPLICATION NUMBER: US/10/750,185  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIN version 3.1  
; SEQ ID NO 47833  
; LENGTH: 874  
; TYPE: DNA  
; ORGANISM: Bovine 19866881262435  
US-10-750-185-47833

Query Match 70.5%; Score 14.8; DB 7; Length 874;  
Best Local Similarity 88.9%; Pred. No. 6.9e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTGCTGTAGTGCGG 19  
|||||  
Db 221 CAAGAGCTGTAGTGAGG 238

## RESULT 35

US-10-750-623-47833  
; Sequence 47833, Application US/10/750,623  
; Publication No. US20050287531A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-1  
; CURRENT APPLICATION NUMBER: US/10/750,623  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIN version 3.1  
; SEQ ID NO 47833  
; LENGTH: 874  
; TYPE: DNA  
; ORGANISM: Bovine 19866881262435  
US-10-750-623-47833

Query Match 70.5%; Score 14.8; DB 7; Length 874;  
Best Local Similarity 88.9%; Pred. No. 6.9e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTGCTGTAGTGCGG 19  
|||||  
Db 221 CAAGAGCTGTAGTGAGG 238

## RESULT 36

US-10-750-185-46874/c  
; Sequence 46874, Application US/10/750,185  
; Publication No. US20050260603A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-2  
; CURRENT APPLICATION NUMBER: US/10/750,185

; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIN version 3.1  
; SEQ ID NO 46874  
; LENGTH: 1187  
; TYPE: DNA  
; ORGANISM: Bovine 19866880774723  
US-10-750-185-46874

Query Match 70.5%; Score 14.8; DB 7; Length 1187;  
Best Local Similarity 88.9%; Pred. No. 7.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTGCTGTAGTGCGG 19  
|||||  
Db 185 CAATGCTATAGTGCGG 168

## RESULT 37

US-10-750-623-46874/c  
; Sequence 46874, Application US/10/750,623  
; Publication No. US20050287531A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-1  
; CURRENT APPLICATION NUMBER: US/10/750,623  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIN version 3.1  
; SEQ ID NO 46874  
; LENGTH: 1187  
; TYPE: DNA  
; ORGANISM: Bovine 19866880774723  
US-10-750-623-46874

Query Match 70.5%; Score 14.8; DB 7; Length 1187;  
Best Local Similarity 88.9%; Pred. No. 7.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTGCTGTAGTGCGG 19  
|||||  
Db 185 CAATGCTATAGTGCGG 168

## RESULT 38

US-10-750-185-46077  
; Sequence 46077, Application US/10/750,185  
; Publication No. US20050260603A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-2  
; CURRENT APPLICATION NUMBER: US/10/750,185  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31

```
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 46077
; LENGTH: 1258
; TYPE: DNA
; ORGANISM: Bovine 19866881551932
US-10-750-185-46077

Query Match          70.5%; Score 14.8; DB 7; Length 1258;
Best Local Similarity 88.9%; Pred. No. 7.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGGTGG 18
    |||||
DB 183 GCAAGTGCTGGAGGTGG 200

RESULT 39
US-10-750-623-46077
; Sequence 46077, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 46077
; LENGTH: 1258
; TYPE: DNA
; ORGANISM: Bovine 19866881551932
US-10-750-623-46077

Query Match          70.5%; Score 14.8; DB 7; Length 1258;
Best Local Similarity 88.9%; Pred. No. 7.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGGTGG 18
    |||||
DB 183 GCAAGTGCTGGAGGTGG 200

RESULT 40
US-10-750-185-63637/c
; Sequence 63637, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 63637
```

```
; LENGTH: 1321
; TYPE: DNA
; ORGANISM: Bovine 19866880725092
US-10-750-185-63637

Query Match          70.5%; Score 14.8; DB 7; Length 1321;
Best Local Similarity 88.9%; Pred. No. 7.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 AGTGCTGTAGGTGCGGG 21
    |||||
DB 838 AGTGGTATAGGTGCGGG 821

RESULT 41
US-10-750-623-63637/c
; Sequence 63637, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 63637
; LENGTH: 1321
; TYPE: DNA
; ORGANISM: Bovine 19866880725092
US-10-750-623-63637

Query Match          70.5%; Score 14.8; DB 7; Length 1321;
Best Local Similarity 88.9%; Pred. No. 7.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 AGTGCTGTAGGTGCGGG 21
    |||||
DB 838 AGTGGTATAGGTGCGGG 821

RESULT 42
US-11-000-688-138/c
; Sequence 138, Application US/11000688
; Publication No. US20050287544A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, Francois
; APPLICANT: HOULGATTE, Remi
; APPLICANT: BIRNEAUM, Daniel
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
; FILE REFERENCE: 1423-R-03
; CURRENT APPLICATION NUMBER: US/11/000,688
; CURRENT FILING DATE: 2004-12-01
; PRIOR APPLICATION NUMBER: US 60/525,987
; PRIOR FILING DATE: 2003-12-01
; NUMBER OF SEQ ID NOS: 1596
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 138
; LENGTH: 1444
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial sequences:primer
; NAME/KEY: misc_feature
```



; LOCATION: (1)..(1444)  
; OTHER INFORMATION: spi-b transcription factor (spi-1/pu.1  
; OTHER INFORMATION: related (SPiB) gene.  
US-11-000-688-138

Query Match 70.5%; Score 14.8; DB 8; Length 1444;  
Best Local Similarity 88.9%; Pred. No. 7.2e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 AGTGCTGTAGTGCGGG 21  
||| ||||| ||||| |||||  
Db 260 AGGGCTGTAGTGCGGG 243

## RESULT 43

US-10-750-185-41819/c  
; Sequence 41819, Application US/10750185  
; Publication No. US20050260603A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-2  
; CURRENT APPLICATION NUMBER: US/10/750,185  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIN version 3.1  
; SEQ ID NO 41819  
; LENGTH: 3331  
; TYPE: DNA  
; ORGANISM: Bovine 19866880995190

US-10-750-185-41819

Query Match 70.5%; Score 14.8; DB 7; Length 3331;  
Best Local Similarity 88.9%; Pred. No. 7.9e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 AGTGCTGTAGTGCGGG 21  
||| ||||| ||||| |||||  
Db 2671 ACTGCTGTAGTGCTGGG 2654

## RESULT 44

US-10-750-623-41819/c  
; Sequence 41819, Application US/10750623  
; Publication No. US20050287531A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-1  
; CURRENT APPLICATION NUMBER: US/10/750,623  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIN version 3.1  
; SEQ ID NO 41819  
; LENGTH: 3331  
; TYPE: DNA  
; ORGANISM: Bovine 19866880995190

## US-10-750-623-41819

Query Match 70.5%; Score 14.8; DB 7; Length 3331;  
Best Local Similarity 88.9%; Pred. No. 7.9e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 AGTGCTGTAGTGCGGG 21  
||| ||||| ||||| |||||  
Db 2671 ACTGCTGTAGTGCTGGG 2654

## RESULT 45

US-10-750-185-52746  
; Sequence 52746, Application US/10750185  
; Publication No. US20050260603A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-2  
; CURRENT APPLICATION NUMBER: US/10/750,185  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIN version 3.1  
; SEQ ID NO 52746  
; LENGTH: 3404  
; TYPE: DNA  
; ORGANISM: Bovine 19866881067975

US-10-750-185-52746

Query Match 70.5%; Score 14.8; DB 7; Length 3404;  
Best Local Similarity 88.9%; Pred. No. 7.9e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 AGTGCTGTAGTGCGGG 21

||| ||||| ||||| |||||

Db 1817 AGTGCTTTAGTGCTGGG 1834

## RESULT 46

US-10-750-623-52746  
; Sequence 52746, Application US/10750623  
; Publication No. US20050287531A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-1  
; CURRENT APPLICATION NUMBER: US/10/750,623  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIN version 3.1  
; SEQ ID NO 52746  
; LENGTH: 3404  
; TYPE: DNA  
; ORGANISM: Bovine 19866881067975

US-10-750-623-52746

Query Match 70.5%; Score 14.8; DB 7; Length 3404;

Best Local Similarity 88.9%; Pred. No. 7.9e+02; Mismatches 2; Indels 0; Gaps 0;

QY 4 AGTGCTGTAGTGGGG 21

Db 1817 AGTGCTGTAGTGGG 1834

RESULT 47

US-10-516-768-22

; Sequence 22, Application US/10516768

; Publication No. US20050256302A1

; GENERAL INFORMATION:

; APPLICANT: MINAMINO, NAOTO

; APPLICANT: KATAFUCHI, TAKESHI

; TITLE OF INVENTION: NOVEL PEPTIDES HAVING CAMP PRODUCING ACTIVITY

; FILE REFERENCE: 62273(71526)

; CURRENT APPLICATION NUMBER: US/10/516,768

; PRIOR FILING DATE: 2004-12-03

; PRIOR APPLICATION NUMBER: PCT/JP03/06641

; PRIOR FILING DATE: 2003-05-28

; PRIOR APPLICATION NUMBER: JP 2002-162797

; NUMBER OF SEQ ID NOS: 52

; SOFTWARE: PatentIn ver. 3.3

; SEQ ID NO 22

; LENGTH: 7142

; TYPE: DNA

; ORGANISM: Sus sp.

US-10-516-768-22

Query Match

Best Local Similarity 70.5%; Score 14.8; DB 7; Length 7142;

Mismatches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAAGTGCTGTAGTGGG 19

Db 5987 CATGTGCTGAGGTGGG 5904

RESULT 48

US-10-995-561-65200

; Sequence 65200, Application US/10995561

; Publication No. US20050272054A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

; FILE REFERENCE: DETECTION AND USES THEREOF

; FILE REFERENCE: CL001559

; CURRENT APPLICATION NUMBER: US/10/995,561

; CURRENT FILING DATE: 2004-11-24

; NUMBER OF SEQ ID NOS: 85702

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 65200

; LENGTH: 201

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-995-561-65200

Query Match

Best Local Similarity 69.5%; Score 14.6; DB 7; Length 201;

Mismatches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGGG 21

Db 104 GGAAGTGCTGAGGGGGGGG 124

RESULT 49

US-10-995-561-82368/c

; Sequence 82368, Application US/10995561

; Publication No. US20050272054A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

; FILE REFERENCE: DETECTION AND USES THEREOF

; FILE REFERENCE: CL001559

; CURRENT APPLICATION NUMBER: US/10/995,561

; CURRENT FILING DATE: 2004-11-24

; NUMBER OF SEQ ID NOS: 85702

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 82368

; LENGTH: 201

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-995-561-82368

Query Match

Best Local Similarity 69.5%; Score 14.6; DB 7; Length 201;

Mismatches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGGG 21

Db 65 GCAGGTGCTGAGGTCCGGTG 45

RESULT 50

US-10-995-561-82380/c

; Sequence 82380, Application US/10995561

; Publication No. US20050272054A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

; FILE REFERENCE: DETECTION AND USES THEREOF

; FILE REFERENCE: CL001559

; CURRENT APPLICATION NUMBER: US/10/995,561

; CURRENT FILING DATE: 2004-11-24

; NUMBER OF SEQ ID NOS: 85702

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 82380

; LENGTH: 201

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-995-561-82380

Query Match

Best Local Similarity 69.5%; Score 14.6; DB 7; Length 201;

Mismatches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGGG 21

Db 33 GCAGGTGCTGAGGTCCGGTG 13

Search completed: January 27, 2006, 07:33:57

Job time : 398 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 27, 2006, 04:45:58 ; Search time 72.5 Seconds  
(without alignments)  
514.880 Million cell updates/sec

Title: US-10-070-415A-1

Perfect score: 21

Sequence: 1 cccgtgaggaactwctgtct 21

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents NA:\*

- 1: /cgn2\_6/prodata1/ina/1 COMB.seq.\*
- 2: /cgn2\_6/prodata1/ina/5 COMB.seq.\*
- 3: /cgn2\_6/prodata1/ina/6A COMB.seq.\*
- 4: /cgn2\_6/prodata1/ina/6B COMB.seq.\*
- 5: /cgn2\_6/prodata1/ina/H COMB.seq.\*
- 6: /cgn2\_6/prodata1/ina/PTUS COMB.seq.\*
- 7: /cgn2\_6/prodata1/ina/PP COMB.seq.\*
- 8: /cgn2\_6/prodata1/ina/RE COMB.seq.\*
- 9: /cgn2\_6/prodata1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20.6	98.1	25	3	US-09-782-361-1
2	20.6	98.1	27	2	US-08-256-568B-1
3	20.6	98.1	27	3	US-09-038-369B-1
4	20.6	98.1	27	3	US-09-378-900A-1
5	20.6	98.1	27	3	US-09-899-044-1
6	20.6	98.1	27	3	US-09-899-302-1
7	20.6	98.1	27	3	US-09-899-082B-1
8	20.6	98.1	28	3	US-08-474-700B-2
9	20.6	98.1	28	3	US-08-474-700B-29
10	20.6	98.1	28	6	PT-US95-05812-2
11	20.6	98.1	28	6	PT-US95-05812-29
12	20.6	98.1	45	2	US-08-690-495-22
13	20.6	98.1	45	3	US-08-690-494-22
14	20.6	98.1	45	2	US-09-299-217-22
15	20.6	98.1	45	3	US-09-728-265-22
16	20.6	98.1	45	3	US-10-309-438-22
17	20.6	98.1	45	6	PT-US95-07671-22
18	20.6	98.1	45	8	US-09-798-641-22
19	20.6	98.1	51	2	US-08-356-287-31
20	20.6	98.1	51	6	PT-US93-04863-31
21	20.6	98.1	67	3	US-08-474-700B-42
22	20.6	98.1	155	3	US-08-474-700B-41
23	20.6	98.1	242	2	US-08-335-595-1
24	20.6	98.1	260	3	US-08-474-700B-40



; FILING DATE: 27-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410,004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 27 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: genomic DNA  
; HYPOTHETICAL: YES  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: HCV (Kato et al., 1992)  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT: HCV  
; MAP POSITION: Position -299 of 5' end  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 1..27  
; OTHER INFORMATION: /standard name=  
; OTHER INFORMATION: "Universal HCV primer HcPr-98"  
US-09-038-3698-1

Query Match 98.1%; Score 20.6; DB 3; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.29;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAAGTCTGTCT 21  
|||||  
Db 1 CCCTGTGAGGAAGTCTGTCT 21

## RESULT 4

US-09-378-900A-1  
; Sequence 1, Application US/09378900A  
; Patent No. 6495670  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; TITLE OF INVENTION: ISOLATES  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/378,900A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/256,568  
; FILING DATE: 18-JUL-1994  
; APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/93/402,129.6  
; FILING DATE: 31-AUG-1993  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP/92/403,222.0  
; FILING DATE: 27-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410,004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 27 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: genomic DNA  
; HYPOTHETICAL: YES  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: HCV (Kato et al., 1992)  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT: HCV  
; MAP POSITION: Position -299 of 5' end  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 1..27  
; OTHER INFORMATION: /standard name=  
; OTHER INFORMATION: "Universal HCV primer HcPr98"  
US-09-378-900A-1

Query Match 98.1%; Score 20.6; DB 3; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.29;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAAGTCTGTCT 21  
|||||  
Db 1 CCCTGTGAGGAAGTCTGTCT 21

## RESULT 5

US-09-899-044-1  
; Sequence 1, Application US/098990044  
; Patent No. 6548244  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; TITLE OF INVENTION: ISOLATES  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/899,044  
; FILING DATE: 06-JUL-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/378,900  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-NOV-1993  
; APPLICATION NUMBER: EP/93/402,129.6  
; FILING DATE: 31-AUG-1993  
; APPLICATION NUMBER: EP/92/403,222.0

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;
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: HCV (Kato et al., 1992)
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: HCV
; MAP POSITION: Position -299 of 5' end
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..27
; OTHER INFORMATION: /standard name=
; "Universal HCV primer HcPr98"
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-899-044-1

Query Match 98.1%; Score 20.6; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
Db 1 CCCTGTGAGGAAGTCTGTCT 21

RESULT 6
US-09-899-302-1
; Sequence 1, Application US/09899302
; Patent No. 6887985
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/899,302
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/378,900
; FILING DATE:
; APPLICATION NUMBER: 08/256,568
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; PRIOR APPLICATION DATA:

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;
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: HCV (Kato et al., 1992)
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: HCV
; MAP POSITION: Position -299 of 5' end
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..27
; OTHER INFORMATION: /standard name=
; OTHER INFORMATION: "Universal HCV primer HcPr98"
US-09-899-302-1

Query Match 98.1%; Score 20.6; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
Db 1 CCCTGTGAGGAAGTCTGTCT 21

RESULT 7
US-09-899-082B-1
; Sequence 1, Application US/09899082B
; Patent No. 6891026
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Process for typing of HCV isolates
; FILE REFERENCE: 2551-111
; CURRENT APPLICATION NUMBER: US/09/899,082B
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 09/378,900
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 09/044,665
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 08/256,568
; PRIOR FILING DATE: 1994-07-18
; PRIOR APPLICATION NUMBER: PCT/EP93/03325
; PRIOR FILING DATE: 1993-11-26
; PRIOR APPLICATION NUMBER: EP92403222
; PRIOR FILING DATE: 1992-11-27
; PRIOR APPLICATION NUMBER: EP93402129
; PRIOR FILING DATE: 1993-08-31
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 27
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: HcPr98
US-09-899-082B-1

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Query Match 98.1%; Score 20.6; DB 3; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.29;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAAGTCTGTCT 21  
Db 1 CCCTGTGAGGAAGTCTGTCT 21

## RESULT 8

US-08-474-700B-2/c  
Sequence 2, Application US/08474700B  
Patent No. 6001990  
GENERAL INFORMATION:  
APPLICANT: Wanda, Jack  
APPLICANT: Wakita, Takaji  
APPLICANT: Moradpour, Darius  
TITLE OF INVENTION: ANTISENSE INHIBITION OF HEPATITIS C  
TITLE OF INVENTION: VIRUS  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,700B  
FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/240,382  
FILING DATE: 10 May 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 00786/279001  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-474-700B-2

Query Match 98.1%; Score 20.6; DB 3; Length 28;  
Best Local Similarity 95.2%; Pred. No. 0.3;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAAGTCTGTCT 21  
Db 23 CCCTGTGAGGAAGTCTGTCT 3

## RESULT 9

US-08-474-700B-29  
Sequence 29, Application US/08474700B  
Patent No. 6001990  
GENERAL INFORMATION:  
APPLICANT: Wanda, Jack  
APPLICANT: Wakita, Takaji  
APPLICANT: Moradpour, Darius  
TITLE OF INVENTION: ANTISENSE INHIBITION OF HEPATITIS C

TITLE OF INVENTION: VIRUS  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,700B  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/240,382  
FILING DATE: 10 May 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 00786/279001  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-474-700B-29

Query Match 98.1%; Score 20.6; DB 3; Length 28;  
Best Local Similarity 95.2%; Pred. No. 0.3;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAAGTCTGTCT 21  
Db 6 CCCTGTGAGGAAGTCTGTCT 26

## RESULT 10

PCT-US95-05812-2/c  
Sequence 2, Application PC/TUS9505812  
GENERAL INFORMATION:  
APPLICANT: Wanda, Jack  
APPLICANT: Wakita, Takaji  
TITLE OF INVENTION: ANTISENSE INHIBITION OF  
HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/05812  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/240,382  
FILING DATE: 10 May 1994

Fri Jan 27 09:12:34 2006

ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00786/221001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
PCT-US95-05812-2

Query Match 98.1%; Score 20.6; DB 6; Length 28;  
Best Local Similarity 95.2%; Pred. No. 0.3;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21  
DB 23 CCCTGTGAGGAAGTCTGTCT 3

RESULT 11  
PCT-US95-05812-29  
Sequence 29, Application PC/TUS9505812  
GENERAL INFORMATION:  
APPLICANT: Wakita, Takaji  
TITLE OF INVENTION: ANTISENSE INHIBITION OF  
TITLE OF INVENTION: HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/05812  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/240,382  
FILING DATE: 10 May 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00786/221001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
PCT-US95-05812-29

Query Match 98.1%; Score 20.6; DB 6; Length 28;  
Best Local Similarity 95.2%; Pred. No. 0.3;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21  
DB 6 CCCTGTGAGGAAGTCTGTCT 26

RESULT 12  
US-08-690-495-22/c  
Sequence 22, Application US/08690495  
Patent No. 5876924  
GENERAL INFORMATION:  
APPLICANT: Zhang, David Y., Brandwein, Margaret  
TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION METHOD:  
TITLE OF INVENTION: HYBRIDIZATION SIGNAL AMPLIFICATION METHOD (HSAM)  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10112-0228  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: FASSEQ Version #1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/690,495  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MacLeod, Janet M. 35,263  
REGISTRATION NUMBER: 35,263  
REFERENCE/DOCKET NUMBER: 29545-A-PCT/USA-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-408-2597  
TELEFAX: 212-765-2519  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..45  
US-08-690-495-22

Query Match 98.1%; Score 20.6; DB 2; Length 45;  
Best Local Similarity 95.2%; Pred. No. 0.32;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21  
DB 31 CCCTGTGAGGAAGTCTGTCT 11

RESULT 13  
US-08-690-494-22/c  
Sequence 22, Application US/08690494  
Patent No. 5942391  
GENERAL INFORMATION:  
APPLICANT: Zhang, David Y., Brandwein, Margaret  
TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION METHOD:  
TITLE OF INVENTION: HYBRIDIZATION SIGNAL AMPLIFICATION METHOD (HSAM)  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: NY  
COUNTRY: USA



ZIP: 10112-0228  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PassSeq Version #1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/690,494  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MacLeod, Janet M.  
REGISTRATION NUMBER: 35,263  
REFERENCE/DOCKET NUMBER: 29545-A-PCT/USA-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-408-2597  
TELEFAX: 212-765-2519  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..45  
US-08-690-494-22

Query Match 98.1%; Score 20.6; DB 2; Length 45;  
Best Local Similarity 95.2%; Pred. No. 0.32;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21  
|||||  
DB 31 CCCTGTGAGGAAGTCTGTCT 11

## RESULT 14

US-09-299-217-22/c  
Sequence 22, Application US/09299217  
Patent No. 6569647

## GENERAL INFORMATION:

APPLICANT: Zhang, David Y., Brandwein, Margaret  
TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION METHOD:  
HYBRIDIZATION SIGNAL AMPLIFICATION METHOD (HSAM)

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10112-0228

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PassSeq Version #1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/299,217

FILING DATE: 23-Apr-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/690,494

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: MacLeod, Janet M.

REGISTRATION NUMBER: 35,263

REFERENCE/DOCKET NUMBER: 29545-A-PCT/USA-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-408-2597

TELEFAX: 212-765-2519

INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..45  
SEQUENCE DESCRIPTION: SEQ ID NO: 22:  
US-09-299-217-22

Query Match 98.1%; Score 20.6; DB 3; Length 45;  
Best Local Similarity 95.2%; Pred. No. 0.32;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21  
|||||  
DB 31 CCCTGTGAGGAAGTCTGTCT 11

## RESULT 15

US-09-728-265-22/c

Sequence 22, Application US/09728265

Patent No. 6593086

GENERAL INFORMATION:

APPLICANT: Zhang, David Y.

TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION METHOD:

TITLE OF INVENTION: RAMIFICATION-EXTENSION AMPLIFICATION METHOD (RAM)

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: Stroock & Stroock & Lavan

STREET: 180 Maiden Lane

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10038

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/728,265

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Pokotilow, Steven B

REGISTRATION NUMBER: 26,405

REFERENCE/DOCKET NUMBER: Old 29545APCT/USA-B // New 251305/0018

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212806-6663

TELEFAX: 2128066006

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 45 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: misc feature

LOCATION: 1..45

US-09-728-265-22

Query Match 98.1%; Score 20.6; DB 3; Length 45;  
Best Local Similarity 95.2%; Pred. No. 0.32;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21  
|||||  
DB 31 CCCTGTGAGGAAGTCTGTCT 11

```

RESULT 16
US-10-309-438-22/c
; Sequence 22, Application US/10309438
; Patent No. 6855523
; GENERAL INFORMATION:
; APPLICANT: Zhang, David Y.
; APPLICANT: Brandwein, Margaret
; APPLICANT: Hsuih, Terence C.H.
; TITLE OF INVENTION: Nucleic Acid Amplification Method: Ramification-extension
; TITLE OF INVENTION: amplification method (RAM)
; FILE REFERENCE: 251305/0031
; CURRENT APPLICATION NUMBER: US/10/309,438
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: US 09/299,217
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: US 08/690,494
; PRIOR FILING DATE: 1996-07-31
; PRIOR APPLICATION NUMBER: US 08/596,331
; PRIOR FILING DATE: 1996-05-20
; PRIOR APPLICATION NUMBER: PCT/US95/07671
; PRIOR FILING DATE: 1995-06-14
; PRIOR APPLICATION NUMBER: 08/263,937
; PRIOR FILING DATE: 1994-06-22
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 22
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide probe
US-10-309-438-22

Query Match          98.1%; Score 20.6; DB 3; Length 45;
Best Local Similarity 95.2%; Pred. No. 0.32;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
Db 31 CCTGTGAGGAAGTCTGTCT 11

RESULT 17
PCT-US95-07671-22/c
; Sequence 22, Application PC/TUS9507671
; GENERAL INFORMATION:
; APPLICANT: Zhang, David Y.
; TITLE OF INVENTION: LIGATION-DEPENDENT AMPLIFICATION FOR THE
; TITLE OF INVENTION: DETECTION OF INFECTIOUS PATHOGENS AND ABNORMAL GENES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10112-0228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07671
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Seide, Rochelle K.
; REGISTRATION NUMBER: 32,300
; REFERENCE/DOCKET NUMBER: 29545-A-PCT
; TELECOMMUNICATION INFORMATION:

```

```

; TELEPHONE: 212-408-2626
; TELEFAX: 212-765-2519
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..45
; PCT-US95-07671-22

Query Match          98.1%; Score 20.6; DB 6; Length 45;
Best Local Similarity 95.2%; Pred. No. 0.32;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
Db 31 CCTGTGAGGAAGTCTGTCT 11

RESULT 18
US-09-798-641-22/c
; Sequence 22, Application US/09798641
; Patent No. RE38442
; GENERAL INFORMATION:
; APPLICANT: Zhang, David Y., Brandwein, Margaret
; TITLE OF INVENTION: HYBRIDIZATION SIGNAL AMPLIFICATION METHOD (HSAM)
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10112-0228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PseSEQ Version #1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/798,641
; FILING DATE: 02-Mar-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,495
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MacLeod, Janet M.
; REGISTRATION NUMBER: 35,263
; REFERENCE/DOCKET NUMBER: 29545-A-PCT/USA-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-408-2597
; TELEFAX: 212-765-2519
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..45
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-798-641-22

Query Match          98.1%; Score 20.6; DB 8; Length 45;
Best Local Similarity 95.2%; Pred. No. 0.32;

```

Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAAGTCTGTCT 21  
 Db 31 CCCTGTGAGGAAGTCTGTCT 11

RESULT 19

US-08-356-287-31  
 ; Sequence 31, Application US/08356287  
 ; Patent No. 5686272  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ronald L. Marshall  
 ; APPLICANT: John J. Carrino  
 ; APPLICANT: Joann Sustachek  
 ; TITLE OF INVENTION: AMPLIFICATION OF RNA SEQUENCES USING  
 ; THE LIGASE CHAIN REACTION  
 ; NUMBER OF SEQUENCES: 36  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Abbott Laboratories  
 ; STREET: 100 Abbott Park Road  
 ; CITY: Abbott Park  
 ; STATE: Illinois  
 ; COUNTRY: USA  
 ; ZIP: 60064-3500  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy diskette  
 ; COMPUTER: Macintosh  
 ; OPERATING SYSTEM: System 7.0.1  
 ; SOFTWARE: Microsoft Word 5.1a  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/356,287  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/891,543  
 ; FILING DATE: 29 MAY 1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Paul D. Vaseger  
 ; REGISTRATION NUMBER: 37,477  
 ; REFERENCE/DOCKET NUMBER: 5172.US.P1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 708-937-2341  
 ; TELEFAX: 708-938-2623  
 ; INFORMATION FOR SEQ ID NO: 31:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 51  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: Other nucleic acid (synthetic DNA)  
 ; US-08-356-287-31

Query Match 98.1%; Score 20.6; DB 2; Length 51;  
 Best Local Similarity 95.2%; Pred. No. 0.33;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAAGTCTGTCT 21  
 Db 16 CCCTGTGAGGAAGTCTGTCT 36

RESULT 20

PCT-US93-04863-31  
 ; Sequence 31, Application PC/TUS9304863  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ronald L. Marshall  
 ; APPLICANT: John J. Carrino  
 ; APPLICANT: Joann C. Sustachek  
 ; TITLE OF INVENTION: AMPLIFICATION OF RNA SEQUENCES  
 ; USING THE LIGASE CHAIN REACTION  
 ; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Abbott Laboratories  
 ; STREET: One Abbott Park Road  
 ; CITY: Abbott Park  
 ; STATE: Illinois  
 ; COUNTRY: USA  
 ; ZIP: 60064-3500  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy diskette  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Wordperfect  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US93/04863  
 ; FILING DATE: 19930524  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/891,543  
 ; FILING DATE: 29 MAY 1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Thomas D. Brainard  
 ; REGISTRATION NUMBER: 32,459  
 ; REFERENCE/DOCKET NUMBER: 5172.PC.01  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 708-937-4884  
 ; TELEFAX: 708-938-2623  
 ; INFORMATION FOR SEQ ID NO: 31:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 51  
 ; TYPE: NUCLEIC ACID  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: Other nucleic acid (synthetic DNA)  
 ; PCT-US93-04863-31

Query Match 98.1%; Score 20.6; DB 6; Length 51;  
 Best Local Similarity 95.2%; Pred. No. 0.33;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAAGTCTGTCT 21  
 Db 16 CCCTGTGAGGAAGTCTGTCT 36

RESULT 21

US-08-474-700B-42/c  
 ; Sequence 42, Application US/08474700B  
 ; Patent No. 6001990  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wands, Jack  
 ; APPLICANT: Wakita, Takaji  
 ; APPLICANT: Moradpour, Darius  
 ; TITLE OF INVENTION: ANTISENSE INHIBITION OF HEPATITIS C  
 ; NUMBER OF SEQUENCES: 45  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Fish & Richardson P.C.  
 ; CITY: Boston  
 ; STATE: Massachusetts  
 ; COUNTRY: U.S.A.  
 ; ZIP: 02110-2804  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; COMPUTER: IBM PS/2 Model 50Z or 55SX  
 ; OPERATING SYSTEM: MS-DOS (Version 5.0)  
 ; SOFTWARE: Wordperfect (Version 5.1)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/474,700B  
 ; FILING DATE: 07-JUN-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/240,382  
 ; FILING DATE: 10 May 1994

ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 00786/279001  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 67 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-474-700B-42

Query Match 98.1%; Score 20.6; DB 3; Length 67;  
Best Local Similarity 95.2%; Pred. No. 0.35; Indels 0; Gaps 0;  
Matches 20; Conservative 1; Mismatches 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21  
|||||  
DB 25 CCCTGTGAGGAAGTCTGTCT 5

RESULT 22  
US-08-474-700B-41/c  
Sequence 41, Application US/08474700B  
Patent No. 6001990  
GENERAL INFORMATION:  
APPLICANT: Wands, Jack  
APPLICANT: Wakita, Takaji  
APPLICANT: Moradpour, Darius  
TITLE OF INVENTION: ANTISENSE INHIBITION OF HEPATITIS C  
TITLE OF INVENTION: VIRUS  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 50Z or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,700B  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/240,382  
FILING DATE: 10 May 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 00786/279001  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 155 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-474-700B-41

Query Match 98.1%; Score 20.6; DB 3; Length 155;

Best Local Similarity 95.2%; Pred. No. 0.41; Indels 0; Gaps 0;  
Matches 20; Conservative 1; Mismatches 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21  
|||||  
DB 113 CCCTGTGAGGAAGTCTGTCT 93

RESULT 23  
US-08-335-595-1  
Sequence 1, Application US/08335595  
Patent No. 5914228  
GENERAL INFORMATION:  
APPLICANT: VIERLING, JOHN M  
APPLICANT: HU, KE-QIN  
TITLE OF INVENTION: DIRECT DETECTION OF HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LYON & LYON  
STREET: 611 WEST 6TH STREET  
CITY: LOS ANGELES  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/335,595  
FILING DATE: 08-NOV-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/175,473  
FILING DATE:  
APPLICATION NUMBER: US/07/758,862  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: SCHNEIDER, CAROL A  
REGISTRATION NUMBER: 34,923  
REFERENCE/DOCKET NUMBER: 194/285  
TELEPHONE: 213-489-1600  
TELEFAX: 213-955-0440  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 242 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-335-595-1

Query Match 98.1%; Score 20.6; DB 2; Length 242;  
Best Local Similarity 95.2%; Pred. No. 0.45; Indels 0; Gaps 0;  
Matches 20; Conservative 1; Mismatches 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21  
|||||  
DB 20 CCCTGTGAGGAAGTCTGTCT 40

RESULT 24  
US-08-474-700B-40/c  
Sequence 40, Application US/08474700B  
Patent No. 6001990  
GENERAL INFORMATION:  
APPLICANT: Wands, Jack  
APPLICANT: Wakita, Takaji  
APPLICANT: Moradpour, Darius  
TITLE OF INVENTION: ANTISENSE INHIBITION OF HEPATITIS C  
TITLE OF INVENTION: VIRUS

; NUMBER OF SEQUENCES: 45  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Fish & Richardson P.C.  
 ; STREET: 225 Franklin Street  
 ; CITY: Boston  
 ; STATE: Massachusetts  
 ; COUNTRY: U.S.A.  
 ; ZIP: 02110-2804  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; COMPUTER: IBM PS/2 Model 502 or 55SX  
 ; OPERATING SYSTEM: MS-DOS (Version 5.0)  
 ; SOFTWARE: WordPerfect (Version 5.1)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/474,700B  
 ; FILING DATE: 07-JUN-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/240,382  
 ; FILING DATE: 10 May 1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Fraser, Janis K.  
 ; REGISTRATION NUMBER: 34,819  
 ; REFERENCE/DOCKET NUMBER: 00786/279001  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (617) 542-5070  
 ; TELEFAX: (617) 542-8906  
 ; TELEX: 200154  
 ; INFORMATION FOR SEQ ID NO: 40:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 260 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA  
 ; US-08-474-700B-40

Query Match 98.1%; Score 20.6; DB 3; Length 260;  
 Best Local Similarity 95.2%; Pred. No. 0.45;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21  
 DB 218 CCCTGTGAGGAAGTCTGTCT 198

RESULT 25  
 US-09-899-082B-98  
 ; Sequence 98, Application US/09899082B  
 ; Patent No. 6891026  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Innogenetics N.V.  
 ; TITLE OF INVENTION: Process for typing of HCV isolates  
 ; FILE REFERENCE: 2551-111  
 ; CURRENT APPLICATION NUMBER: US/09/899,082B  
 ; CURRENT FILING DATE: 2001-07-06  
 ; PRIOR APPLICATION NUMBER: 09/378,900  
 ; PRIOR FILING DATE: 1999-08-23  
 ; PRIOR APPLICATION NUMBER: 09/044,665  
 ; PRIOR FILING DATE: 1998-03-19  
 ; PRIOR APPLICATION NUMBER: 08/256,568  
 ; PRIOR FILING DATE: 1994-07-18  
 ; PRIOR APPLICATION NUMBER: PCT/EP93/03325  
 ; PRIOR FILING DATE: 1993-11-26  
 ; PRIOR APPLICATION NUMBER: EP92403222  
 ; PRIOR FILING DATE: 1992-11-27  
 ; PRIOR APPLICATION NUMBER: EP93402129  
 ; PRIOR FILING DATE: 1993-08-31  
 ; NUMBER OF SEQ ID NOS: 128  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 98  
 ; LENGTH: 260  
 ; TYPE: DNA  
 ; ORGANISM: hepatitis C virus

US-09-899-082B-98  
 Query Match 98.1%; Score 20.6; DB 3; Length 260;  
 Best Local Similarity 95.2%; Pred. No. 0.45;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CCCTGTGAGGAAGTCTGTCT 21  
 DB 17 CCCTGTGAGGAAGTCTGTCT 37

RESULT 26  
 US-09-899-082B-99  
 ; Sequence 99, Application US/09899082B  
 ; Patent No. 6891026  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Innogenetics N.V.  
 ; TITLE OF INVENTION: Process for typing of HCV isolates  
 ; FILE REFERENCE: 2551-111  
 ; CURRENT APPLICATION NUMBER: US/09/899,082B  
 ; CURRENT FILING DATE: 2001-07-06  
 ; PRIOR APPLICATION NUMBER: 09/378,900  
 ; PRIOR FILING DATE: 1999-08-23  
 ; PRIOR APPLICATION NUMBER: 09/044,665  
 ; PRIOR FILING DATE: 1998-03-19  
 ; PRIOR APPLICATION NUMBER: 08/256,568  
 ; PRIOR FILING DATE: 1994-07-18  
 ; PRIOR APPLICATION NUMBER: PCT/EP93/03325  
 ; PRIOR FILING DATE: 1993-11-26  
 ; PRIOR APPLICATION NUMBER: EP92403222  
 ; PRIOR FILING DATE: 1992-11-27  
 ; PRIOR APPLICATION NUMBER: EP93402129  
 ; PRIOR FILING DATE: 1993-08-31  
 ; NUMBER OF SEQ ID NOS: 128  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 99  
 ; LENGTH: 260  
 ; TYPE: DNA  
 ; ORGANISM: hepatitis C virus  
 ; US-09-899-082B-99

Query Match 98.1%; Score 20.6; DB 3; Length 260;  
 Best Local Similarity 95.2%; Pred. No. 0.45;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21  
 DB 17 CCCTGTGAGGAAGTCTGTCT 37

RESULT 27  
 US-09-899-082B-100  
 ; Sequence 100, Application US/09899082B  
 ; Patent No. 6891026  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Innogenetics N.V.  
 ; TITLE OF INVENTION: Process for typing of HCV isolates  
 ; FILE REFERENCE: 2551-111  
 ; CURRENT APPLICATION NUMBER: US/09/899,082B  
 ; CURRENT FILING DATE: 2001-07-06  
 ; PRIOR APPLICATION NUMBER: 09/378,900  
 ; PRIOR FILING DATE: 1999-08-23  
 ; PRIOR APPLICATION NUMBER: 09/044,665  
 ; PRIOR FILING DATE: 1998-03-19  
 ; PRIOR APPLICATION NUMBER: 08/256,568  
 ; PRIOR FILING DATE: 1994-07-18  
 ; PRIOR APPLICATION NUMBER: PCT/EP93/03325  
 ; PRIOR FILING DATE: 1993-11-26  
 ; PRIOR APPLICATION NUMBER: EP92403222  
 ; PRIOR FILING DATE: 1992-11-27  
 ; PRIOR APPLICATION NUMBER: EP93402129  
 ; PRIOR FILING DATE: 1993-08-31  
 ; NUMBER OF SEQ ID NOS: 128

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 100
; LENGTH: 260
; TYPE: DNA
; ORGANISM: hepatitis C virus
US-09-899-082B-100

Query Match          98.1%; Score 20.6; DB 3; Length 260;
Best Local Similarity 95.2%; Pred. No. 0.45;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
   |||||
DB 17 CCCTGTGAGGAAGTCTGTCT 37

RESULT 28
US-09-899-082B-101
; Sequence 101, Application US/09899082B
; Patent No. 6891026
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Process for typing of HCV isolates
; FILE REFERENCE: 2551-111
; CURRENT APPLICATION NUMBER: US/09/899,082B
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 09/378,900
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 09/044,665
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 08/256,568
; PRIOR FILING DATE: 1994-07-18
; PRIOR APPLICATION NUMBER: PCT/EP93/03325
; PRIOR FILING DATE: 1993-11-26
; PRIOR APPLICATION NUMBER: EP92403222
; PRIOR FILING DATE: 1992-11-27
; PRIOR APPLICATION NUMBER: EP93402129
; PRIOR FILING DATE: 1993-08-31
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
; LENGTH: 260
; TYPE: DNA
; ORGANISM: hepatitis C virus
US-09-899-082B-101

Query Match          98.1%; Score 20.6; DB 3; Length 260;
Best Local Similarity 95.2%; Pred. No. 0.45;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
   |||||
DB 17 CCCTGTGAGGAAGTCTGTCT 37

RESULT 29
US-08-332-616A-1
; Sequence 1, Application US/08332616A
; Patent No. 5620852
; GENERAL INFORMATION:
; APPLICANT: LIN, LILY
; APPLICANT: CIMINO, GEORGE
; APPLICANT: ZHU, YU SHENG
; TITLE OF INVENTION: NUCLEIC ACID PREPARATION METHODS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,616A
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,545
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: HRI-01202
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 305 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-332-616A-1

Query Match          98.1%; Score 20.6; DB 2; Length 305;
Best Local Similarity 95.2%; Pred. No. 0.47;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
   |||||
DB 43 CCCTGTGAGGAAGTCTGTCT 63

RESULT 30
US-08-317-220-1
; Sequence 1, Application US/08317220
; Patent No. 5654179
; GENERAL INFORMATION:
; APPLICANT: LIN, LILY
; TITLE OF INVENTION: NUCLEIC ACID PREPARATION METHODS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PETER G. CARROLL
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,220
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/044,649
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,545
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: HRI-00542
```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 305 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-317-220-1

Query Match          98.1%; Score 20.6; DB 2; Length 305;
Best Local Similarity 95.2%; Pred. No. 0.47;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
Db 43 CCCTGTGAGGAAGTCTGTCT 63

RESULT 31
US-08-444-818-108
; Sequence 108, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,818
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,590
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harbin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)359-3876
; TELEFAX: (508)359-3885
; INFORMATION FOR SEQ ID NO: 108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 308 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ANTI-SENSE: YES
; IMMEDIATE SOURCE:
; CLONE: 18g
US-08-444-818-108

Query Match          98.1%; Score 20.6; DB 3; Length 308;
Best Local Similarity 95.2%; Pred. No. 0.47;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
Db 43 CCCTGTGAGGAAGTCTGTCT 63

```

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Db 19 CCCTGTGAGGAAGTCTGTCT 39

RESULT 32
US-08-444-818-109/c
; Sequence 109, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,818
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,590
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harbin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)359-3876
; TELEFAX: (508)359-3885
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 308 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ANTI-SENSE: YES
; IMMEDIATE SOURCE:
; CLONE: 18g
US-08-444-818-109

Query Match          98.1%; Score 20.6; DB 3; Length 308;
Best Local Similarity 95.2%; Pred. No. 0.47;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
Db 290 CCCTGTGAGGAAGTCTGTCT 270

RESULT 33
US-08-444-818-110
; Sequence 110, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA

```

```

; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,818
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,590
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harbin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)359-3876
; TELEFAX: (508)359-3885
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 308 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; IMMEDIATE SOURCE:
; CLONE: 189
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..72
; US-08-444-818-110

Query Match 98.1%; Score 20.6; DB 3; Length 308;
Best Local Similarity 95.2%; Pred. No. 0.47;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
Db 19 CCCTGTGAGGAAGTCTGTCT 39

RESULT 34
US-08-444-818-112
; Sequence 112, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,818
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,590
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harbin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)359-3876
; TELEFAX: (508)359-3885
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 308 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; IMMEDIATE SOURCE:
; CLONE: 189

```

```

; NAME: Harbin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)359-3876
; TELEFAX: (508)359-3885
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 308 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; IMMEDIATE SOURCE:
; CLONE: 189
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..55
; US-08-444-818-112

Query Match 98.1%; Score 20.6; DB 3; Length 308;
Best Local Similarity 95.2%; Pred. No. 0.47;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
Db 19 CCCTGTGAGGAAGTCTGTCT 39

RESULT 35
US-08-444-818-114
; Sequence 114, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,818
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,590
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harbin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)359-3876
; TELEFAX: (508)359-3885
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 308 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; IMMEDIATE SOURCE:
; CLONE: 189

```



FEATURE:  
NAME/KEY: CDS  
LOCATION: 72..116  
US-08-444-818-114

Query Match 98.1%; Score 20.6; DB 3; Length 308;  
Best Local Similarity 95.2%; Pred. No. 0.47;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21  
Db 19 CCTGTGAGGAAGTCTGTCT 39

RESULT 36

US-08-444-818-116  
Sequence 116, Application US/08444818  
Patent No. 6150087  
GENERAL INFORMATION:  
APPLICANT: Chien, David Y.  
TITLE OF INVENTION: NANBV Diagnostics and Vaccines  
NUMBER OF SEQUENCES: 777  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/444,818  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/403,590  
FILING DATE: 14-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Harbin, Alisa A.  
REGISTRATION NUMBER: 33,895  
REFERENCE/DOCKET NUMBER: 0110.002  
TELEPHONE: (508)359-3876  
TELEFAX: (508)359-3885  
INFORMATION FOR SEQ ID NO: 116:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 308 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: 189  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 191..226  
US-08-444-818-116

Query Match 98.1%; Score 20.6; DB 3; Length 308;  
Best Local Similarity 95.2%; Pred. No. 0.47;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21  
Db 19 CCTGTGAGGAAGTCTGTCT 39

RESULT 37

US-08-444-818-118  
Sequence 118, Application US/08444818  
Patent No. 6150087  
GENERAL INFORMATION:  
APPLICANT: Chien, David Y.  
TITLE OF INVENTION: NANBV Diagnostics and Vaccines  
NUMBER OF SEQUENCES: 777  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/444,818  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/403,590  
FILING DATE: 14-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Harbin, Alisa A.  
REGISTRATION NUMBER: 33,895  
REFERENCE/DOCKET NUMBER: 0110.002  
TELEPHONE: (508)359-3876  
TELEFAX: (508)359-3885  
INFORMATION FOR SEQ ID NO: 118:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 308 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: 189  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 276..308  
US-08-444-818-118

Query Match 98.1%; Score 20.6; DB 3; Length 308;  
Best Local Similarity 95.2%; Pred. No. 0.47;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21  
Db 19 CCTGTGAGGAAGTCTGTCT 39

RESULT 38

US-08-470-426B-1  
Sequence 1, Application US/08470426B  
Patent No. 5856458  
GENERAL INFORMATION:  
APPLICANT: Okamoto, Hiroaki  
TITLE OF INVENTION: OLIGONUCLEOTIDE PRIMERS, AND THEIR  
APPLICATION FOR HIGH-FIDELITY DETECTION OF NON-A, NON-B  
HEPATITIS VIRUS  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Beveridge, DeGrandi, Weilacher & Young,  
STREET: 1850 M Street, N.W., Suite 800  
CITY: Washington

```

; STATE: DC
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-153402
; FILING DATE: 12-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weillacher, Robert G.
; REGISTRATION NUMBER: 20,531
; REFERENCE/DOCKET NUMBER: 06/59-47083.1
; TELEPHONE: (202) 659-2811
; TELEFAX: (202) 659-1462
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 324 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; US-08-470-426B-1

Query Match          98.1%; Score 20.6; DB 2; Length 324;
Best Local Similarity 95.2%; Pred. No. 0.47;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
Db 26 CCCTGTGAGGAAGTCTGTCT 46

RESULT 39
US-08-470-426B-15
; Sequence 15, Application US/08470426B
; Patent No. 5856458
; GENERAL INFORMATION:
; APPLICANT: Okamoto, Hiroaki
; APPLICANT: Nakamura, Tetuo
; TITLE OF INVENTION: OLIGONUCLEOTIDE PRIMERS, AND THEIR
; TITLE OF INVENTION: APPLICATION FOR HIGH-FIDELITY DETECTION OF NON-A, NON-B
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Beveridge, DeGrandi, Weillacher & Young,
; ADDRESSEE: L.L.P.
; STREET: 1850 M Street, N.W., Suite 800
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,426B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-153402
; FILING DATE: 12-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weillacher, Robert G.

```

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; REGISTRATION NUMBER: 20,531
; REFERENCE/DOCKET NUMBER: 06/59-47083.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 659-2811
; TELEFAX: (202) 659-1462
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 324 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; US-08-470-426B-15

Query Match          98.1%; Score 20.6; DB 2; Length 324;
Best Local Similarity 95.2%; Pred. No. 0.47;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
Db 26 CCCTGTGAGGAAGTCTGTCT 46

RESULT 40
US-08-440-209-1
; Sequence 1, Application US/08440209
; Patent No. 5922857
; GENERAL INFORMATION:
; APPLICANT: Han, Jang H
; APPLICANT: Spaete, Richard R
; TITLE OF INVENTION: Methods and Compositions for Controlling
; TITLE OF INVENTION: Translation of HCV Proteins
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield, and Sacks P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,209
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/477,895
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: US 08/128,583
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Janiuk, Anthony J
; REGISTRATION NUMBER: 29,809
; REFERENCE/DOCKET NUMBER: C0772/7004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 341 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: ns5hcv1
; US-08-440-209-1

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Query Match          98.1%; Score 20.6; DB 2; Length 341;
Best Local Similarity 95.2%; Pred. No. 0.48;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
DB 43 CCCTGTGAGGAAGTCTGTCT 63

RESULT 41
US-08-854-531-4
; Sequence 4, Application US/08854531
; Patent No. 6025341
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack
; APPLICANT: Tokushige, Katsutoshi
; APPLICANT: Wakita, Takaji
; TITLE OF INVENTION: CHIMERIC HEPATITIS B/HEPATITIS C VIRUS VACCINE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6025341ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,531
; FILING DATE: Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: APOL-0214
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 341 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-854-531-4

Query Match          98.1%; Score 20.6; DB 3; Length 341;
Best Local Similarity 95.2%; Pred. No. 0.48;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
DB 43 CCCTGTGAGGAAGTCTGTCT 63

RESULT 42
US-08-439-996-1
; Sequence 1, Application US/08439996
; Patent No. 6057093
; GENERAL INFORMATION:
; APPLICANT: Han, Jang H
; APPLICANT: Spaete, Richard R
; TITLE OF INVENTION: Methods and Compositions for Controlling
; NUMBER OF INVENTION: Translation of HCV Proteins
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield, and Sacks P.C.
; STREET: 600 Atlantic Avenue

Query Match          98.1%; Score 20.6; DB 2; Length 341;
Best Local Similarity 95.2%; Pred. No. 0.48;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
DB 43 CCCTGTGAGGAAGTCTGTCT 63

RESULT 43
US-09-014-416-47
; Sequence 47, Application US/09014416
; Patent No. 6153421
; GENERAL INFORMATION:
; APPLICANT: Yanagi, Masayuki
; APPLICANT: Bukh, Jens
; APPLICANT: Emerson, Susanne U.
; APPLICANT: Purcell, Robert H.
; TITLE OF INVENTION: CLONED GENOMES OF INFECTIOUS HEPATITIS C VIRUSES AND
; FILE REFERENCE: 20264276
; CURRENT APPLICATION NUMBER: US/09/014,416
; CURRENT FILING DATE: 1998-01-27
; EARLIER APPLICATION NUMBER: US 60/053,062
; EARLIER FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 341
; TYPE: DNA
; ORGANISM: Hepatitis C virus
; US-09-014-416-47

Query Match          98.1%; Score 20.6; DB 3; Length 341;
Best Local Similarity 95.2%; Pred. No. 0.48;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
DB 43 CCCTGTGAGGAAGTCTGTCT 63

RESULT 44
US-09-014-416-47
; Sequence 47, Application US/09014416
; Patent No. 6153421
; GENERAL INFORMATION:
; APPLICANT: Yanagi, Masayuki
; APPLICANT: Bukh, Jens
; APPLICANT: Emerson, Susanne U.
; APPLICANT: Purcell, Robert H.
; TITLE OF INVENTION: CLONED GENOMES OF INFECTIOUS HEPATITIS C VIRUSES AND
; FILE REFERENCE: 20264276
; CURRENT APPLICATION NUMBER: US/09/014,416
; CURRENT FILING DATE: 1998-01-27
; EARLIER APPLICATION NUMBER: US 60/053,062
; EARLIER FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 341
; TYPE: DNA
; ORGANISM: Hepatitis C virus
; US-09-014-416-47
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Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21  
 Db 43 CCCTGTGAGGAAGTCTGTCT 63

RESULT 44

US-09-014-416-48  
 ; Sequence 48, Application US/09014416  
 ; Patent No. 6153421  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yanagi, Masayuki  
 ; APPLICANT: Bukh, Jens  
 ; APPLICANT: Emerson, Susanne U.  
 ; APPLICANT: Purcell, Robert H.  
 ; TITLE OF INVENTION: CLONED GENOMES OF INFECTIOUS HEPATITIS C VIRUSES AND  
 ; TITLE OF INVENTION: USES THEREOF  
 ; FILE REFERENCE: 20264276  
 ; CURRENT APPLICATION NUMBER: US/09/014,416  
 ; CURRENT FILING DATE: 1998-01-27  
 ; EARLIER APPLICATION NUMBER: US 60/053,062  
 ; EARLIER FILING DATE: 1997-07-18  
 ; NUMBER OF SEQ ID NOS: 65  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 48  
 ; LENGTH: 341  
 ; TYPE: DNA  
 ; ORGANISM: Hepatitis C virus  
 ; ORGANISM: Hepatitis C virus  
 ; ORGANISM: Hepatitis C virus

Query Match 98.1%; Score 20.6; DB 3; Length 341;  
 Best Local Similarity 95.2%; Pred. No. 0.48;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21  
 Db 43 CCCTGTGAGGAAGTCTGTCT 63

RESULT 45

US-09-014-416-49  
 ; Sequence 49, Application US/09014416  
 ; Patent No. 6153421  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yanagi, Masayuki  
 ; APPLICANT: Bukh, Jens  
 ; APPLICANT: Emerson, Susanne U.  
 ; APPLICANT: Purcell, Robert H.  
 ; TITLE OF INVENTION: CLONED GENOMES OF INFECTIOUS HEPATITIS C VIRUSES AND  
 ; TITLE OF INVENTION: USES THEREOF  
 ; FILE REFERENCE: 20264276  
 ; CURRENT APPLICATION NUMBER: US/09/014,416  
 ; CURRENT FILING DATE: 1998-01-27  
 ; EARLIER APPLICATION NUMBER: US 60/053,062  
 ; EARLIER FILING DATE: 1997-07-18  
 ; NUMBER OF SEQ ID NOS: 65  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 49  
 ; LENGTH: 341  
 ; TYPE: DNA  
 ; ORGANISM: Hepatitis C virus  
 ; ORGANISM: Hepatitis C virus  
 ; ORGANISM: Hepatitis C virus

Query Match 98.1%; Score 20.6; DB 3; Length 341;  
 Best Local Similarity 95.2%; Pred. No. 0.48;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21  
 Db 43 CCCTGTGAGGAAGTCTGTCT 63

RESULT 46

US-08-869-380-4  
 ; Sequence 4, Application US/08869380  
 ; Patent No. 6235888  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pachuk, Catherine J.  
 ; APPLICANT: Wands, Jack  
 ; APPLICANT: Wakita, Takaji  
 ; APPLICANT: Zurawski, Jr., Vincent R.  
 ; APPLICANT: Coney, Leslie R.  
 ; TITLE OF INVENTION: Hepatitis C Virus Vaccine  
 ; NUMBER OF SEQUENCES: 7  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &  
 ; ADDRESSEE: No. 6235888ris  
 ; STREET: One Liberty Place, 46th floor  
 ; CITY: Philadelphia  
 ; STATE: PA  
 ; COUNTRY: USA  
 ; ZIP: 19103  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/869,380  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/318,248  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Deluca, Mark  
 ; REGISTRATION NUMBER: 33,229  
 ; REFERENCE/DOCKET NUMBER: APOL-0189  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (215) 568-3100  
 ; TELEFAX: (215) 568-3439  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 341 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; Molecule Type: cDNA  
 ; US-08-869-380-4

Query Match 98.1%; Score 20.6; DB 3; Length 341;  
 Best Local Similarity 95.2%; Pred. No. 0.48;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21  
 Db 43 CCCTGTGAGGAAGTCTGTCT 63

RESULT 47

US-09-814-351-3  
 ; Sequence 3, Application US/09814351  
 ; Patent No. 6692736  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yu, De-Chao  
 ; APPLICANT: Li, Yuanhao  
 ; APPLICANT: Henderson, Daniel R.  
 ; TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTORS  
 ; TITLE OF INVENTION: COMPRISING AN INTERNAL RIBOSOME ENTRY SITE  
 ; FILE REFERENCE: 348022001700  
 ; CURRENT APPLICATION NUMBER: US/09/814,351  
 ; CURRENT FILING DATE: 2001-03-21  
 ; PRIOR APPLICATION NUMBER: 60/192,156  
 ; PRIOR FILING DATE: 2000-03-24  
 ; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 341  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: 5' UTR region of HCV  
US-09-814-351-3

Query Match 98.1%; Score 20.6; DB 3; Length 341;  
Best Local Similarity 95.2%; Pred. No. 0.48;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGAACTACTGTCT 21  
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Db 43 CCCTGTGAGGAAGAACTACTGTCT 63

## RESULT 48

US-09-814-292-44  
; Sequence 44, Application US/09814292  
; Patent No. 6852528  
; GENERAL INFORMATION:  
; APPLICANT: Yu, De-Chao  
; APPLICANT: Zhang, Hong  
; APPLICANT: Henderson, Daniel R.  
; TITLE OF INVENTION: HUMAN UROTHELIAL CELL SPECIFIC UROPLAKIN  
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATORY SEQUENCES, VECTORS COMPRISING  
; TITLE OF INVENTION: UROPLAKIN-SPECIFIC TRANSCRIPTIONAL REGULATORY SEQUENCES, AND  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 348022001500  
; CURRENT APPLICATION NUMBER: US/09/814,292  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: 60/191,861  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 44  
; LENGTH: 341  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: 5' UTR region of HCV  
US-09-814-292-44

Query Match 98.1%; Score 20.6; DB 3; Length 341;  
Best Local Similarity 95.2%; Pred. No. 0.48;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGAACTACTGTCT 21  
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Db 43 CCCTGTGAGGAAGAACTACTGTCT 63

## RESULT 49

US-09-814-357-3  
; Sequence 3, Application US/09814357  
; Patent No. 6911200  
; GENERAL INFORMATION:  
; APPLICANT: Yu, De-Chao  
; APPLICANT: Chen, Yu  
; APPLICANT: Henderson, Daniel R.  
; TITLE OF INVENTION: METHODS OF TREATING NEOPLASIA  
; TITLE OF INVENTION: WITH COMBINATION TARGET CELL-SPECIFIC ADENOVIRUS,  
; TITLE OF INVENTION: CHEMOTHERAPY AND RADIATION  
; FILE REFERENCE: 348022001600  
; CURRENT APPLICATION NUMBER: US/09/814,357  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 60/192,015  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3

; LENGTH: 341  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: 5' UTR region of HCV  
US-09-814-357-3

Query Match 98.1%; Score 20.6; DB 3; Length 341;  
Best Local Similarity 95.2%; Pred. No. 0.48;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGAACTACTGTCT 21  
|||||  
Db 43 CCCTGTGAGGAAGAACTACTGTCT 63

## RESULT 50

US-10-259-275-35  
; Sequence 35, Application US/10259275  
; Patent No. 6921634  
; GENERAL INFORMATION:  
; APPLICANT: Lemon, Stanley M.  
; APPLICANT: Yi, Minkyung  
; TITLE OF INVENTION: REPLICATION COMPETENT HEPATITIS C VIRUS AND METHODS OF USE  
; FILE REFERENCE: 265.0007 0120  
; CURRENT APPLICATION NUMBER: US/10/259,275  
; CURRENT FILING DATE: 2003-01-13  
; PRIOR APPLICATION NUMBER: US 60/171,909  
; PRIOR FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: US 09/747,419  
; PRIOR FILING DATE: 2000-12-23  
; PRIOR APPLICATION NUMBER: US 60/325,236  
; PRIOR FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: US 60/338,123  
; PRIOR FILING DATE: 2001-11-13  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 35  
; LENGTH: 341  
; TYPE: DNA  
; ORGANISM: ARTIFICIAL  
; FEATURE:  
; OTHER INFORMATION: nucleotide sequence of 5' NTR  
US-10-259-275-35

Query Match 98.1%; Score 20.6; DB 3; Length 341;  
Best Local Similarity 95.2%; Pred. No. 0.48;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGAACTACTGTCT 21  
|||||  
Db 43 CCCTGTGAGGAAGAACTACTGTCT 63

Search completed: January 27, 2006, 07:08:53  
Job time : 73.5 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 27, 2006, 05:37:30 ; Search time 348.5 Seconds  
(without alignments)  
498.298 Million cell updates/sec

Title: US-10-070-415A-37\_COPY\_410\_430

Perfect score: 21

Sequence: 1 gcaagtgtgtaggtgcggg 21

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Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*  
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7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*  
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10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	20	95.2	581	7	US-10-070-415A-16
3	20	95.2	581	7	US-10-070-415A-17
4	20	95.2	581	7	US-10-070-415A-18
5	20	95.2	581	7	US-10-070-415A-19
6	19.4	92.4	581	3	US-09-813-031-1
7	19.4	92.4	581	3	US-09-813-031-2
8	19.4	92.4	581	3	US-09-813-031-3
9	19.4	92.4	581	3	US-09-813-031-4
10	19.4	92.4	581	3	US-09-813-990A-1
11	19.4	92.4	581	3	US-09-813-990A-2
12	19.4	92.4	581	3	US-09-813-990A-3
13	19.4	92.4	581	3	US-09-813-990A-4
14	19.4	92.4	581	7	US-10-070-415A-38
15	19.4	92.4	581	7	US-10-070-415A-39
16	19.4	92.4	581	7	US-10-070-415A-40
17	19.4	92.4	581	9	US-10-633-659-1
18	19.4	92.4	581	9	US-10-633-659-2
19	19.4	92.4	581	9	US-10-633-659-3
20	19.4	92.4	581	9	US-10-633-659-4
21	19.4	92.4	2451	8	US-10-492-396-5
22	19.4	92.4	5376	8	US-10-492-396-7
23	17.8	84.8	752	7	US-10-424-599-60215

24	17.8	84.8	5981	6	US-10-311-455-2165	Sequence 2165, Ap
25	17	81.0	3302	3	US-09-968-007A-992	Sequence 992, Ap
26	17	81.0	3302	7	US-10-755-889-357	Sequence 357, App
27	17	81.0	3302	9	US-10-843-641A-7462	Sequence 7462, Ap
28	17	81.0	3302	9	US-10-887-553A-335	Sequence 335, App
29	17	81.0	3579	5	US-10-198-846-11469	Sequence 11469, A
30	16.8	80.0	565	9	US-10-972-079-13406	Sequence 13406, A
31	16.8	80.0	595	9	US-10-972-079-13405	Sequence 13405, A
32	16.8	80.0	954	9	US-10-450-763-29555	Sequence 29555, A
33	16.8	80.0	1840	9	US-10-450-763-17672	Sequence 17672, A
34	16.8	80.0	2178	9	US-10-450-763-17668	Sequence 17668, A
35	16.8	80.0	2179	9	US-10-450-763-25501	Sequence 25501, A
36	16.8	80.0	2250	9	US-10-450-763-29558	Sequence 29558, A
37	16.8	80.0	2830	9	US-10-450-763-29562	Sequence 29562, A
38	16.8	80.0	3039	9	US-10-450-763-25465	Sequence 25465, A
39	16.8	80.0	3039	9	US-10-450-763-29044	Sequence 29044, A
40	16.8	80.0	3039	9	US-10-450-763-29143	Sequence 29143, A
41	16.8	80.0	3355	9	US-10-450-763-21560	Sequence 21560, A
42	16.8	80.0	4134	3	US-09-815-242-6287	Sequence 6287, Ap
43	16.8	80.0	4134	6	US-10-287-274-296	Sequence 296, App
44	16.8	80.0	4134	7	US-10-282-122A-6547	Sequence 6547, Ap
45	16.8	80.0	4194	7	US-10-282-122A-6875	Sequence 6875, Ap
46	16.8	80.0	4236	7	US-10-282-122A-6876	Sequence 6876, Ap
47	16.8	80.0	5471	9	US-10-450-763-26014	Sequence 26014, A
48	16.8	80.0	5519	5	US-10-114-170-226	Sequence 226, App
49	16.8	80.0	9072	2	US-08-781-986A-45	Sequence 45, Appl
50	16.8	80.0	9072	7	US-10-329-624-45	Sequence 45, Appl
51	16.2	77.1	520	5	US-10-027-632-287754	Sequence 287754, A
52	16.2	77.1	520	6	US-10-027-632-287754	Sequence 287754, A
53	16.2	77.1	590	4	US-09-925-065A-545841	Sequence 545841, A
54	16.2	77.1	610	4	US-09-925-065A-630591	Sequence 630591, A
55	16.2	77.1	760	5	US-10-027-632-145547	Sequence 145547, A
56	16.2	77.1	760	6	US-10-027-632-145547	Sequence 145547, A
57	16.2	77.1	786	8	US-10-435-115-67484	Sequence 67484, A
58	16.2	77.1	945	9	US-10-511-278-89	Sequence 89, Appl
59	16.2	77.1	948	8	US-10-774-355A-126	Sequence 126, App
60	16.2	77.1	954	6	US-10-029-386-24933	Sequence 24933, A
61	16.2	77.1	989	6	US-10-024-212-39	Sequence 39, Appl
62	16.2	77.1	995	6	US-10-035-806-31	Sequence 31, Appl
63	16.2	77.1	1110	6	US-10-411-224-11	Sequence 11, Appl
64	16.2	77.1	1110	6	US-10-047-021-11	Sequence 11, Appl
65	16.2	77.1	1110	9	US-10-970-493-11	Sequence 11, Appl
66	16.2	77.1	1146	9	US-10-450-763-7562	Sequence 7562, Ap
67	16.2	77.1	1282	6	US-10-305-720-1413	Sequence 1413, Ap
68	16.2	77.1	1324	7	US-10-260-238-1698	Sequence 1698, Ap
69	16.2	77.1	1481	8	US-10-739-930-5282	Sequence 5282, Ap
70	16.2	77.1	1668	7	US-10-425-114-2656	Sequence 2656, Ap
71	16.2	77.1	1751	8	US-10-425-115-1393	Sequence 1393, Ap
72	16.2	77.1	2746	8	US-10-739-930-4188	Sequence 4188, Ap
73	16.2	77.1	3009	6	US-10-369-493-25065	Sequence 25065, A
74	16.2	77.1	3280	7	US-10-437-963-73692	Sequence 73692, A
75	16.2	77.1	3492	7	US-10-437-963-93329	Sequence 93329, A
76	16.2	77.1	5519	9	US-10-887-553A-684	Sequence 684, App
77	16.2	77.1	11771	9	US-10-415-620-1	Sequence 1, Appl
78	16.2	77.1	25760	3	US-09-999-121-13	Sequence 13, Appl
79	16.2	77.1	42823	8	US-10-643-801-18	Sequence 18, Appl
80	16.2	77.1	52799	7	US-10-322-281-630	Sequence 630, App
81	16.2	77.1	347001	7	US-10-319-908-16	Sequence 16, Appl
82	16	76.2	25	8	US-10-719-900-299123	Sequence 299123, A
83	15.8	75.2	201	8	US-10-719-993-17805	Sequence 17805, A
84	15.8	75.2	236	6	US-09-796-692-6242	Sequence 6242, Ap
85	15.8	75.2	236	5	US-10-040-862-6242	Sequence 6242, Ap
86	15.8	75.2	236	6	US-10-057-475B-6242	Sequence 6242, Ap
87	15.8	75.2	236	6	US-10-154-884B-6242	Sequence 6242, Ap
88	15.8	75.2	236	8	US-10-784-324-6242	Sequence 6242, Ap
89	15.8	75.2	286	7	US-10-424-599-133670	Sequence 133670, A
90	15.8	75.2	340	3	US-09-867-701-4147	Sequence 4147, Ap
91	15.8	75.2	399	4	US-09-925-065A-239953	Sequence 239953, A
92	15.8	75.2	543	3	US-09-933-561-9	Sequence 9, Appl
93	15.8	75.2	559	3	US-10-487-901-5512	Sequence 5512, Ap
94	15.8	75.2	600	9	US-10-972-079-34586	Sequence 34586, A
95	15.8	75.2	661	9	US-10-487-901-5513	Sequence 5513, Ap
96	15.8	75.2	681	7	US-10-437-963-33361	Sequence 33361, A

97 15.8 75.2 696 5 US-10-027-632-136957 Sequence 136957,  
 98 15.8 75.2 696 6 US-10-027-632-136957 Sequence 136957,  
 99 15.8 75.2 777 7 US-10-260-238-4421 Sequence 4421, Ap  
 c 100 15.8 75.2 1028 7 US-10-437-963-3037 Sequence 3037, Ap

# ALIGNMENTS

RESULT 1  
 US-10-070-415A-37  
 ; Sequence 37, Application US/10070415A  
 ; Publication No. US20040043379A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HASHIMOTO, Koji  
 ; APPLICANT: ASHIMOTO, Michie  
 ; APPLICANT: MISHIRO, Shunji  
 ; APPLICANT: OOTA, Yasuhiko  
 ; TITLE OF INVENTION: DETECTION OF NUCLEIC ACID ASSOCIATED WITH DISEASE  
 ; FILE REFERENCE: 220633US2SRDPT  
 ; CURRENT APPLICATION NUMBER: US/10/070,415A  
 ; CURRENT FILING DATE: 2003-07-23  
 ; PRIOR APPLICATION NUMBER: PCT/JP02/02030  
 ; PRIOR FILING DATE: 2002-03-05  
 ; PRIOR APPLICATION NUMBER: JP 2001-090053  
 ; PRIOR FILING DATE: 2001-03-27  
 ; PRIOR APPLICATION NUMBER: JP 2001-284112  
 ; PRIOR FILING DATE: 2001-09-18  
 ; NUMBER OF SEQ ID NOS: 72  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 37  
 ; LENGTH: 581  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (455)..(455)  
 ; OTHER INFORMATION: n is one nucleotide selected from a, g, c, or t  
 US-10-070-415A-37

Query Match 100.0%; Score 21; DB 7; Length 581;  
 Best Local Similarity 100.0%; Pred. No. 4.5; Indels 0; Gaps 0;  
 Matches 21; Conservative 0; Mismatches 0;

QY 1 GCAAGTGCTGTAGTGGCGGG 21  
 |||||  
 Db 410 GCAAGTGCTGTAGTGGCGGG 430

RESULT 2  
 US-10-070-415A-16  
 ; Sequence 16, Application US/10070415A  
 ; Publication No. US20040043379A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HASHIMOTO, Koji  
 ; APPLICANT: ASHIMOTO, Michie  
 ; APPLICANT: MISHIRO, Shunji  
 ; APPLICANT: OOTA, Yasuhiko  
 ; TITLE OF INVENTION: DETECTION OF NUCLEIC ACID ASSOCIATED WITH DISEASE  
 ; FILE REFERENCE: 220633US2SRDPT  
 ; CURRENT APPLICATION NUMBER: US/10/070,415A  
 ; CURRENT FILING DATE: 2003-07-23  
 ; PRIOR APPLICATION NUMBER: PCT/JP02/02030  
 ; PRIOR FILING DATE: 2002-03-05  
 ; PRIOR APPLICATION NUMBER: JP 2001-090053  
 ; PRIOR FILING DATE: 2001-03-27  
 ; PRIOR APPLICATION NUMBER: JP 2001-284112  
 ; PRIOR FILING DATE: 2001-09-18  
 ; NUMBER OF SEQ ID NOS: 72  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 16  
 ; LENGTH: 581  
 ; TYPE: DNA

; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (420)..(420)  
 ; OTHER INFORMATION: n is one nucleotide selected from a, g, c, or t  
 US-10-070-415A-16

Query Match 95.2%; Score 20; DB 7; Length 581;  
 Best Local Similarity 95.2%; Pred. No. 13;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGCGGG 21  
 |||||  
 Db 410 GCAAGTGCTGTAGTGGCGGG 430

RESULT 3  
 US-10-070-415A-17  
 ; Sequence 17, Application US/10070415A  
 ; Publication No. US20040043379A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HASHIMOTO, Koji  
 ; APPLICANT: ASHIMOTO, Michie  
 ; APPLICANT: MISHIRO, Shunji  
 ; APPLICANT: OOTA, Yasuhiko  
 ; TITLE OF INVENTION: DETECTION OF NUCLEIC ACID ASSOCIATED WITH DISEASE  
 ; FILE REFERENCE: 220633US2SRDPT  
 ; CURRENT APPLICATION NUMBER: US/10/070,415A  
 ; CURRENT FILING DATE: 2003-07-23  
 ; PRIOR APPLICATION NUMBER: PCT/JP02/02030  
 ; PRIOR FILING DATE: 2002-03-05  
 ; PRIOR APPLICATION NUMBER: JP 2001-090053  
 ; PRIOR FILING DATE: 2001-03-27  
 ; PRIOR APPLICATION NUMBER: JP 2001-284112  
 ; PRIOR FILING DATE: 2001-09-18  
 ; NUMBER OF SEQ ID NOS: 72  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 17  
 ; LENGTH: 581  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (420)..(420)  
 ; OTHER INFORMATION: n is any nucleotide selected from a, g, c, or t  
 US-10-070-415A-17

Query Match 95.2%; Score 20; DB 7; Length 581;  
 Best Local Similarity 95.2%; Pred. No. 13;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGCGGG 21  
 |||||  
 Db 410 GCAAGTGCTGTAGTGGCGGG 430

RESULT 4  
 US-10-070-415A-18  
 ; Sequence 18, Application US/10070415A  
 ; Publication No. US20040043379A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HASHIMOTO, Koji  
 ; APPLICANT: ASHIMOTO, Michie  
 ; APPLICANT: MISHIRO, Shunji  
 ; APPLICANT: OOTA, Yasuhiko  
 ; TITLE OF INVENTION: DETECTION OF NUCLEIC ACID ASSOCIATED WITH DISEASE  
 ; FILE REFERENCE: 220633US2SRDPT  
 ; CURRENT APPLICATION NUMBER: US/10/070,415A  
 ; CURRENT FILING DATE: 2003-07-23  
 ; PRIOR APPLICATION NUMBER: PCT/JP02/02030  
 ; PRIOR FILING DATE: 2002-03-05  
 ; PRIOR APPLICATION NUMBER: JP 2001-090053  
 ; PRIOR FILING DATE: 2001-03-27



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; PRIOR APPLICATION NUMBER: JP 2001-284112
; PRIOR FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 581
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (420)..(420)
; OTHER INFORMATION: n is any nucleotide selected from a, g, c, or t
US-10-070-415A-18

Query Match          95.2%; Score 20; DB 7; Length 581;
Best Local Similarity 95.2%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 21
Db 410 GCAAGTGTCTAGGTGCGGG 430

RESULT 5
US-10-070-415A-19
; Sequence 19, Application US/10070415A
; Publication No. US20040043379A1
; GENERAL INFORMATION:
; APPLICANT: HASHIMOTO, Koji
; APPLICANT: ASHIMOTO, Michie
; APPLICANT: MISHIRO, Shunji
; APPLICANT: OOTA, Yasuhiko
; TITLE OF INVENTION: DETECTION OF NUCLEIC ACID ASSOCIATED WITH DISEASE
; FILE REFERENCE: 220633US2SRDPT
; CURRENT APPLICATION NUMBER: US/10/070,415A
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: PCT/JP02/02030
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: JP 2001-090053
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: JP 2001-284112
; PRIOR FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 581
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (420)..(420)
; OTHER INFORMATION: n is any nucleotide selected from a, g, c, or t
US-10-070-415A-19

Query Match          95.2%; Score 20; DB 7; Length 581;
Best Local Similarity 95.2%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 21
Db 410 GCAAGTGTCTAGGTGCGGG 430

RESULT 6
US-09-813-031-1
; Sequence 1, Application US/09813031
; Patent No. US20020048758A1
; GENERAL INFORMATION:
; APPLICANT: Hijikata, Minako
; APPLICANT: Mishiro, Shunji
; APPLICANT: Oota, Yasuhiko
; APPLICANT: Hashimoto, Koji
; TITLE OF INVENTION: CARRIER FOR GENE DETECTION AND ITS USE FOR DETECTING VALIDITY OF
; FILE REFERENCE: 205058US0SRD
; CURRENT APPLICATION NUMBER: US/09/813,031

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; TITLE OF INVENTION: INTERFERON THERAPY
; FILE REFERENCE: 205058US0SRD
; CURRENT APPLICATION NUMBER: US/09/813,031
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: JP2000-080955
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: JP2001-062372
; PRIOR FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 581
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-813-031-1

Query Match          92.4%; Score 19.4; DB 3; Length 581;
Best Local Similarity 95.2%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 21
Db 410 GCAAGTGTCTAGGTGCGGG 430

RESULT 7
US-09-813-031-2
; Sequence 2, Application US/09813031
; Patent No. US20020048758A1
; GENERAL INFORMATION:
; APPLICANT: Hijikata, Minako
; APPLICANT: Mishiro, Shunji
; APPLICANT: Oota, Yasuhiko
; APPLICANT: Hashimoto, Koji
; TITLE OF INVENTION: CARRIER FOR GENE DETECTION AND ITS USE FOR DETECTING VALIDITY OF
; FILE REFERENCE: 205058US0SRD
; CURRENT APPLICATION NUMBER: US/09/813,031
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: JP2000-080955
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: JP2001-062372
; PRIOR FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 581
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-813-031-2

Query Match          92.4%; Score 19.4; DB 3; Length 581;
Best Local Similarity 95.2%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 21
Db 410 GCAAGTGTCTAGGTGCGGG 430

RESULT 8
US-09-813-031-3
; Sequence 3, Application US/09813031
; Patent No. US20020048758A1
; GENERAL INFORMATION:
; APPLICANT: Hijikata, Minako
; APPLICANT: Mishiro, Shunji
; APPLICANT: Oota, Yasuhiko
; APPLICANT: Hashimoto, Koji
; TITLE OF INVENTION: CARRIER FOR GENE DETECTION AND ITS USE FOR DETECTING VALIDITY OF
; FILE REFERENCE: 205058US0SRD
; CURRENT APPLICATION NUMBER: US/09/813,031

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; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: JP2000-080955
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: JP2001-062372
; PRIOR FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 581
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-813-031-3
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Query Match 92.4%; Score 19.4; DB 3; Length 581;
Best Local Similarity 95.2%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 GCAAGTGCTGTAGTGGGG 21
| | | | | | | | | | | | | | | | | | | | | |
DB 410 GCAAGTGCTGMAGGTGGGG 430
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RESULT 9
US-09-813-031-4
; Sequence 4, Application US/09813031
; Patent No. US2002048758A1
; GENERAL INFORMATION:
; APPLICANT: Hijikata, Minako
; APPLICANT: Mishiro, Shunji
; APPLICANT: Oota, Yasuhiko
; APPLICANT: Hashimoto, Koji
; TITLE OF INVENTION: CARRIER FOR GENE DETECTION AND ITS USE FOR DETECTING VALIDITY OF
; FILE REFERENCE: 205058US0SRD
; CURRENT APPLICATION NUMBER: US/09/813,031
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: JP2000-080955
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: JP2001-062372
; PRIOR FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 581
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-813-031-4
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Query Match 92.4%; Score 19.4; DB 3; Length 581;
Best Local Similarity 95.2%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 GCAAGTGCTGTAGTGGGG 21
| | | | | | | | | | | | | | | | | | | | | |
DB 410 GCAAGTGCTGMAGGTGGGG 430
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```
RESULT 10
US-09-813-990A-1
; Sequence 1, Application US/09813990A
; Patent No. US20020127558A1
; GENERAL INFORMATION:
; APPLICANT: HIJIKATA, MINAKO
; APPLICANT: MISHIRO, SHUNJI
; APPLICANT: OOTA, YASUHIKO
; APPLICANT: HASHIMOTO, KOJI
; TITLE OF INVENTION: GENETIC POLYMORPHISM OF MXA PROTEIN AND USE THEREOF
; FILE REFERENCE: 205057US0SRD
; CURRENT APPLICATION NUMBER: US/09/813,990A
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: JP2000-080955
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: JP2001-062371
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; PRIOR FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 581
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-813-990A-1
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Query Match 92.4%; Score 19.4; DB 3; Length 581;
Best Local Similarity 95.2%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 GCAAGTGCTGTAGTGGGG 21
| | | | | | | | | | | | | | | | | | | | | |
DB 410 GCAAGTGCTGMAGGTGGGG 430
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RESULT 11
US-09-813-990A-2
; Sequence 2, Application US/09813990A
; Patent No. US20020127558A1
; GENERAL INFORMATION:
; APPLICANT: HIJIKATA, MINAKO
; APPLICANT: MISHIRO, SHUNJI
; APPLICANT: OOTA, YASUHIKO
; APPLICANT: HASHIMOTO, KOJI
; TITLE OF INVENTION: GENETIC POLYMORPHISM OF MXA PROTEIN AND USE THEREOF
; FILE REFERENCE: 205057US0SRD
; CURRENT APPLICATION NUMBER: US/09/813,990A
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: JP2000-080955
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: JP2001-062371
; PRIOR FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 581
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-813-990A-2
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Query Match 92.4%; Score 19.4; DB 3; Length 581;
Best Local Similarity 95.2%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 GCAAGTGCTGTAGTGGGG 21
| | | | | | | | | | | | | | | | | | | | | |
DB 410 GCAAGTGCTGMAGGTGGGG 430
```

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RESULT 12
US-09-813-990A-3
; Sequence 3, Application US/09813990A
; Patent No. US20020127558A1
; GENERAL INFORMATION:
; APPLICANT: HIJIKATA, MINAKO
; APPLICANT: MISHIRO, SHUNJI
; APPLICANT: OOTA, YASUHIKO
; APPLICANT: HASHIMOTO, KOJI
; TITLE OF INVENTION: GENETIC POLYMORPHISM OF MXA PROTEIN AND USE THEREOF
; FILE REFERENCE: 205057US0SRD
; CURRENT APPLICATION NUMBER: US/09/813,990A
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: JP2000-080955
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: JP2001-062371
; PRIOR FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 581
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; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-813-990A-3

Query Match 92.4%; Score 19.4; DB 3; Length 581;  
Best Local Similarity 95.2%; Pred. No. 26;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGGTGCGGG 21  
|||||  
Db 410 GCAAGTGCTGTAGGTGCGGG 430

## RESULT 13

US-09-813-990A-4  
; Sequence 4, Application US/09813990A  
; Patent No. US20020127558A1  
; GENERAL INFORMATION:  
; APPLICANT: HJIUKATA, MINAKO  
; APPLICANT: MISHIRO, SHUNJI  
; APPLICANT: OOTA, YASUHIKO  
; APPLICANT: HASHIMOTO, KOJI  
; TITLE OF INVENTION: GENETIC POLYMORPHISM OF MXA PROTEIN AND USE THEREOF  
; FILE REFERENCE: 205057US0SRD  
; CURRENT APPLICATION NUMBER: US/09/813,990A  
; CURRENT FILING DATE: 2001-03-22  
; PRIOR APPLICATION NUMBER: JP2000-080955  
; PRIOR FILING DATE: 2000-03-22  
; PRIOR APPLICATION NUMBER: JP2001-062371  
; PRIOR FILING DATE: 2001-03-06  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; TYPE: DNA  
; LENGTH: 581  
; ORGANISM: Homo sapiens  
US-09-813-990A-4

Query Match 92.4%; Score 19.4; DB 3; Length 581;  
Best Local Similarity 95.2%; Pred. No. 26;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGGTGCGGG 21  
|||||  
Db 410 GCAAGTGCTGTAGGTGCGGG 430

## RESULT 14

US-10-070-415A-38  
; Sequence 38, Application US/10070415A  
; Publication No. US20040043379A1  
; GENERAL INFORMATION:  
; APPLICANT: HASHIMOTO, Koji  
; APPLICANT: ASHIMOTO, Michie  
; APPLICANT: MISHIRO, Shunji  
; APPLICANT: OOTA, Yasuhiko  
; TITLE OF INVENTION: DETECTION OF NUCLEIC ACID ASSOCIATED WITH DISEASE  
; FILE REFERENCE: 220633US2SRDPT  
; CURRENT APPLICATION NUMBER: US/10/070,415A  
; CURRENT FILING DATE: 2003-07-23  
; PRIOR APPLICATION NUMBER: PCT/JP02/02030  
; PRIOR FILING DATE: 2002-03-05  
; PRIOR APPLICATION NUMBER: JP 2001-090053  
; PRIOR FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: JP 2001-284112  
; PRIOR FILING DATE: 2001-09-18  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 38  
; LENGTH: 581  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:

; NAME/KEY: misc.feature  
; LOCATION: (455)..(455)  
; OTHER INFORMATION: n is one nucleotide selected from a, g, c, or t  
US-10-070-415A-38

Query Match 92.4%; Score 19.4; DB 7; Length 581;  
Best Local Similarity 95.2%; Pred. No. 26;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGGTGCGGG 21  
|||||  
Db 410 GCAAGTGCTGTAGGTGCGGG 430

## RESULT 15

US-10-070-415A-39  
; Sequence 39, Application US/10070415A  
; Publication No. US20040043379A1  
; GENERAL INFORMATION:  
; APPLICANT: HASHIMOTO, Koji  
; APPLICANT: ASHIMOTO, Michie  
; APPLICANT: MISHIRO, Shunji  
; APPLICANT: OOTA, Yasuhiko  
; TITLE OF INVENTION: DETECTION OF NUCLEIC ACID ASSOCIATED WITH DISEASE  
; FILE REFERENCE: 220633US2SRDPT  
; CURRENT APPLICATION NUMBER: US/10/070,415A  
; CURRENT FILING DATE: 2003-07-23  
; PRIOR APPLICATION NUMBER: PCT/JP02/02030  
; PRIOR FILING DATE: 2002-03-05  
; PRIOR APPLICATION NUMBER: JP 2001-090053  
; PRIOR FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: JP 2001-284112  
; PRIOR FILING DATE: 2001-09-18  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 39  
; LENGTH: 581  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (455)..(455)  
; OTHER INFORMATION: n is a nucleotide selected from a, g, c, or t  
US-10-070-415A-39

Query Match 92.4%; Score 19.4; DB 7; Length 581;  
Best Local Similarity 95.2%; Pred. No. 26;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGGTGCGGG 21  
|||||  
Db 410 GCAAGTGCTGTAGGTGCGGG 430

## RESULT 16

US-10-070-415A-40  
; Sequence 40, Application US/10070415A  
; Publication No. US20040043379A1  
; GENERAL INFORMATION:  
; APPLICANT: HASHIMOTO, Koji  
; APPLICANT: ASHIMOTO, Michie  
; APPLICANT: MISHIRO, Shunji  
; APPLICANT: OOTA, Yasuhiko  
; TITLE OF INVENTION: DETECTION OF NUCLEIC ACID ASSOCIATED WITH DISEASE  
; FILE REFERENCE: 220633US2SRDPT  
; CURRENT APPLICATION NUMBER: US/10/070,415A  
; CURRENT FILING DATE: 2003-07-23  
; PRIOR APPLICATION NUMBER: PCT/JP02/02030  
; PRIOR FILING DATE: 2002-03-05  
; PRIOR APPLICATION NUMBER: JP 2001-090053  
; PRIOR FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: JP 2001-284112  
; PRIOR FILING DATE: 2001-09-18

```

; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 581
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (455)..(455)
; OTHER INFORMATION: n is a nucleotide selected from a, g, c, or t
US-10-070-415A-40

Query Match          92.4%; Score 19.4; DB 7; Length 581;
Best Local Similarity 95.2%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGGGG 21
   |||||
Db 410 GCAAGTGCTGCAGGTGGGG 430

RESULT 17
US-10-633-659-1
; Sequence 1, Application US/10633659
; Publication No. US20050100909A1
; GENERAL INFORMATION:
; APPLICANT: Hijikata, Minako
; APPLICANT: Mishiro, Shunji
; APPLICANT: Oota, Yasuhiko
; APPLICANT: Hashimoto, Koji
; TITLE OF INVENTION: CARRIER FOR GENE DETECTION AND ITS USE FOR DETECTING VALIDITY OF
; TITLE OF INVENTION: INTERFERON THERAPY
; FILE REFERENCE: 205058US0SRD
; CURRENT APPLICATION NUMBER: US/10/633,659
; CURRENT FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: US/09/813,031
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: JP2000-080955
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: JP2001-062372
; PRIOR FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 581
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-633-659-1

Query Match          92.4%; Score 19.4; DB 9; Length 581;
Best Local Similarity 95.2%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGGGG 21
   |||||
Db 410 GCAAGTGCTGMAGGTGGGGG 430

RESULT 18
US-10-633-659-2
; Sequence 2, Application US/10633659
; Publication No. US20050100909A1
; GENERAL INFORMATION:
; APPLICANT: Hijikata, Minako
; APPLICANT: Mishiro, Shunji
; APPLICANT: Oota, Yasuhiko
; APPLICANT: Hashimoto, Koji
; TITLE OF INVENTION: CARRIER FOR GENE DETECTION AND ITS USE FOR DETECTING VALIDITY OF
; TITLE OF INVENTION: INTERFERON THERAPY
; FILE REFERENCE: 205058US0SRD
; CURRENT APPLICATION NUMBER: US/10/633,659
; CURRENT FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: US/09/813,031

```

```

; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: JP2000-080955
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: JP2001-062372
; PRIOR FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 581
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-633-659-2

Query Match          92.4%; Score 19.4; DB 9; Length 581;
Best Local Similarity 95.2%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGGGG 21
   |||||
Db 410 GCAAGTGCTGMAGGTGGGGG 430

RESULT 19
US-10-633-659-3
; Sequence 3, Application US/10633659
; Publication No. US20050100909A1
; GENERAL INFORMATION:
; APPLICANT: Hijikata, Minako
; APPLICANT: Mishiro, Shunji
; APPLICANT: Oota, Yasuhiko
; APPLICANT: Hashimoto, Koji
; TITLE OF INVENTION: CARRIER FOR GENE DETECTION AND ITS USE FOR DETECTING VALIDITY OF
; TITLE OF INVENTION: INTERFERON THERAPY
; FILE REFERENCE: 205058US0SRD
; CURRENT APPLICATION NUMBER: US/10/633,659
; CURRENT FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: US/09/813,031
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: JP2000-080955
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: JP2001-062372
; PRIOR FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 581
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-633-659-3

Query Match          92.4%; Score 19.4; DB 9; Length 581;
Best Local Similarity 95.2%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGGGGG 21
   |||||
Db 410 GCAAGTGCTGMAGGTGGGGG 430

RESULT 20
US-10-633-659-4
; Sequence 4, Application US/10633659
; Publication No. US20050100909A1
; GENERAL INFORMATION:
; APPLICANT: Hijikata, Minako
; APPLICANT: Mishiro, Shunji
; APPLICANT: Oota, Yasuhiko
; APPLICANT: Hashimoto, Koji
; TITLE OF INVENTION: CARRIER FOR GENE DETECTION AND ITS USE FOR DETECTING VALIDITY OF
; TITLE OF INVENTION: INTERFERON THERAPY
; FILE REFERENCE: 205058US0SRD
; CURRENT APPLICATION NUMBER: US/10/633,659
; CURRENT FILING DATE: 2003-08-05

```

; PRIOR APPLICATION NUMBER: US/09/813,031  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: JP2000-080955  
; PRIOR FILING DATE: 2000-03-22  
; PRIOR APPLICATION NUMBER: JP2001-062372  
; PRIOR FILING DATE: 2001-03-06  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 581  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-633-659-4

Query Match 92.4%; Score 19.4; DB 9; Length 581;  
Best Local Similarity 95.2%; Pred. No. 26;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCTGTAGTGGGG 21  
|||||  
DB 410 GCAAGTCTGTAGTGGGG 430

## RESULT 21

US-10-492-396-5  
; Sequence 5, Application US/10492396  
; Publication No. US20040209800A1  
; GENERAL INFORMATION:  
; APPLICANT: MUSHINSKI, J F  
; APPLICANT: TREPEL, JANE B  
; APPLICANT: HORISBERGER, MICHEL A  
; APPLICANT: NGUYEN, PHUONGMAI  
; APPLICANT: CHANG, KHANNA  
; TITLE OF INVENTION: USE OF Mx GTPases IN THE PROGNOSIS AND TREATMENT OF CANCER  
; FILE REFERENCE: 403025  
; CURRENT APPLICATION NUMBER: US/10/492,396  
; CURRENT FILING DATE: 2004-04-09  
; PRIOR APPLICATION NUMBER: PCT/US02/33232  
; PRIOR FILING DATE: 2002-10-18  
; PRIOR APPLICATION NUMBER: US 60/329,740  
; PRIOR FILING DATE: 2001-10-18  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-492-396-5

Query Match 92.4%; Score 19.4; DB 8; Length 2451;  
Best Local Similarity 95.2%; Pred. No. 27;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCTGTAGTGGGG 21  
|||||  
DB 2398 GCAAGTCTGTAGTGGGG 2418

## RESULT 22

US-10-492-396-7  
; Sequence 7, Application US/10492396  
; Publication No. US20040209800A1  
; GENERAL INFORMATION:  
; APPLICANT: MUSHINSKI, J F  
; APPLICANT: TREPEL, JANE B  
; APPLICANT: HORISBERGER, MICHEL A  
; APPLICANT: NGUYEN, PHUONGMAI  
; APPLICANT: CHANG, KHANNA  
; TITLE OF INVENTION: USE OF Mx GTPases IN THE PROGNOSIS AND TREATMENT OF CANCER  
; FILE REFERENCE: 403025  
; CURRENT APPLICATION NUMBER: US/10/492,396  
; CURRENT FILING DATE: 2004-04-09  
; PRIOR APPLICATION NUMBER: PCT/US02/33232

; PRIOR FILING DATE: 2002-10-18  
; PRIOR APPLICATION NUMBER: US 60/329,740  
; PRIOR FILING DATE: 2001-10-18  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 5376  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-492-396-7

Query Match 92.4%; Score 19.4; DB 8; Length 5376;  
Best Local Similarity 95.2%; Pred. No. 28;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCTGTAGTGGGG 21  
|||||  
DB 444 GCAAGTCTGTAGTGGGG 464

## RESULT 23

US-10-424-599-60215  
; Sequence 60215, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J  
; APPLICANT: Kovalic, David K  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 60215  
; LENGTH: 752  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(752)  
; OTHER INFORMATION: unsure at all n locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_25386C.1  
US-10-424-599-60215

Query Match 84.8%; Score 17.8; DB 7; Length 752;  
Best Local Similarity 90.5%; Pred. No. 1.5e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTCTGTAGTGGGG 21  
|||||  
DB 615 GCAAGTCTGTAGTGGGG 635

## RESULT 24

US-10-311-455-2165  
; Sequence 2165, Application US/10311455  
; Publication No. US20030143606A1  
; GENERAL INFORMATION:  
; APPLICANT: OLEK, Alexander  
; APPLICANT: PIEPENBROCK, Christian  
; APPLICANT: BERLIN, Kurt  
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Dete  
; FILE REFERENCE: 5013.1014  
; CURRENT APPLICATION NUMBER: US/10/311,455  
; CURRENT FILING DATE: 2002-12-16  
; PRIOR APPLICATION NUMBER: PCT/EP01/07537  
; PRIOR FILING DATE: 2001-07-02

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; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 2165
; LENGTH: 5981
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-2165

Query Match      84.8%; Score 17.8; DB 6; Length 5981;
Best Local Similarity 90.5%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  GCAAGTCTGTAGTGC GGGG 21
Db      4867  GTAAGTGTGTAGTGC GGGG 4887

RESULT 25
US-09-968-007A-992/c
; Sequence 992, Application US/09968007A
; Publication No. US20040115625A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signa
; FILE OF INVENTION: Gene Sets
; FILE REFERENCE: 689290-71
; CURRENT APPLICATION NUMBER: US/09/968,007A
; CURRENT FILING DATE: 2001-10-02
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/60/237,172
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,173
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,278
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,294
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,295
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,316
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 1001
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 992
; LENGTH: 3302
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-968-007A-992

Query Match      81.0%; Score 17; DB 3; Length 3302;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5  GTGCTGTAGTGC GGGG 21
Db      541  GTGCTGTAGTGC GGGG 525

RESULT 26
US-10-755-889-357/c
; Sequence 357, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB
; FILE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
```

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; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 357
; LENGTH: 3302
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION: n=a,t,g or c
US-10-755-889-357

Query Match      81.0%; Score 17; DB 7; Length 3302;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5  GTGCTGTAGTGC GGGG 21
Db      541  GTGCTGTAGTGC GGGG 525

RESULT 27
US-10-843-641A-7462/c
; Sequence 7462, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; FILE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7462
; LENGTH: 3302
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)_(3302)
; OTHER INFORMATION: n=a,t,g or c
US-10-843-641A-7462

Query Match      81.0%; Score 17; DB 9; Length 3302;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5  GTGCTGTAGTGC GGGG 21
Db      541  GTGCTGTAGTGC GGGG 525
```

## RESULT 28

US-10-887-553A-335/c  
; Sequence 335, Application US/10887553A  
; Publication No. US20050085436A1

GENERAL INFORMATION:  
; APPLICANT: Garza, Dan  
; APPLICANT: Li, Hao  
; TITLE OF INVENTION: Method to treat conditions associated with insulin signalling dysregulation  
; FILE REFERENCE: 4-33262  
; CURRENT APPLICATION NUMBER: US/10/887,553A  
; CURRENT FILING DATE: 2004-07-08

PRIOR APPLICATION NUMBER: 60/485,883

PRIOR FILING DATE: 2003-08-07

NUMBER OF SEQ ID NOS: 1208

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 335

LENGTH: 3302

TYPE: DNA

ORGANISM: human

US-10-887-553A-335

Query Match 81.0%; Score 17; DB 9; Length 3302;

Best Local Similarity 100.0%; Pred. No. 3.8e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGGGG 21

Db 541 GTGCTGTAGTGGGGG 525

## RESULT 29

US-10-198-846-11469/c

; Sequence 11469, Application US/10198846

; Publication No. US20030099974A1

GENERAL INFORMATION:

; APPLICANT: Lillie, James

; APPLICANT: Xu, Yongyao

; APPLICANT: Wang, Youzhen

; APPLICANT: Steinmann, Kathleen

; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS

; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND

; TITLE OF INVENTION: THERAPY OF BREAST CANCER

; FILE REFERENCE: MRI-049

; CURRENT APPLICATION NUMBER: US/10/198,846

; CURRENT FILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: 60/306,220

PRIOR FILING DATE: 2001-07-18

NUMBER OF SEQ ID NOS: 14084

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 11469

LENGTH: 3579

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

LOCATION: 3559..3560, 3561, 3562, 3563, 3564, 3565, 3566, 3567, 3568,

LOCATION: 3569, 3570, 3571, 3572, 3573, 3574, 3575, 3576, 3577, 3578,

LOCATION: 3579

OTHER INFORMATION: n = A,T,C or G

US-10-198-846-11469

Query Match

Best Local Similarity 81.0%; Score 17; DB 5; Length 3579;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGGGG 21

Db 628 GTGCTGTAGTGGGGG 612

## RESULT 30

US-10-450-763-29555/c

; Sequence 29555, Application US/10450763

; Publication No. US20050196754A1

US-10-972-079-13406

; Sequence 13406, Application US/10972079

; Publication No. US20050153317A1

GENERAL INFORMATION:

; APPLICANT: MMI GENOMICS, INC.

; APPLICANT: Denise, Sue K.

; APPLICANT: ROSENFELD, David

; APPLICANT: KERR, Richard

; APPLICANT: BATES, Stephen

; APPLICANT: HOLM, Tom

; TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BE

; TITLE OF INVENTION: LIVESTOCK

; FILE REFERENCE: MM1110-2

; CURRENT APPLICATION NUMBER: US/10/972,079

; CURRENT FILING DATE: 2004-10-22

PRIOR APPLICATION NUMBER: US 60/514,333

PRIOR FILING DATE: 2003-10-24

NUMBER OF SEQ ID NOS: 96631

SOFTWARE: PatentIn version 3.1

SEQ ID NO 13406

LENGTH: 565

TYPE: DNA

ORGANISM: Chicken 19866894217856\_4

US-10-972-079-13406

Query Match

Best Local Similarity 80.0%; Score 16.8; DB 9; Length 565;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTGTAGTGGGG 20

Db 486 GCAAGTGTGTAGTGGGG 505

## RESULT 31

US-10-972-079-13405

; Sequence 13405, Application US/10972079

; Publication No. US20050153317A1

GENERAL INFORMATION:

; APPLICANT: MMI GENOMICS, INC.

; APPLICANT: Denise, Sue K.

; APPLICANT: ROSENFELD, David

; APPLICANT: KERR, Richard

; APPLICANT: BATES, Stephen

; APPLICANT: HOLM, Tom

; TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BE

; TITLE OF INVENTION: LIVESTOCK

; FILE REFERENCE: MM1110-2

; CURRENT APPLICATION NUMBER: US/10/972,079

; CURRENT FILING DATE: 2004-10-22

PRIOR APPLICATION NUMBER: US 60/514,333

PRIOR FILING DATE: 2003-10-24

NUMBER OF SEQ ID NOS: 96631

SOFTWARE: PatentIn version 3.1

SEQ ID NO 13405

LENGTH: 595

TYPE: DNA

ORGANISM: Chicken 19866894217856\_3

US-10-972-079-13405

Query Match

Best Local Similarity 80.0%; Score 16.8; DB 9; Length 595;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTGTAGTGGGG 20

Db 516 GCAAGTGTGTAGTGGGG 535

## RESULT 34



RESULT 36  
US-10-450-763-29558/c  
; Sequence 29558, Application US/10450763  
; Publication No. US20050196754A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 790CIP3/US  
; CURRENT APPLICATION NUMBER: US/10/450,763  
; PRIOR FILING DATE: 2003-06-11  
; PRIOR APPLICATION NUMBER: PCT/US01/08631  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
; SEQ ID NO 29558  
; LENGTH: 2250  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIMILAR  
; LOCATION: (1207)..(2208)  
; OTHER INFORMATION: 98% homologous to Escherichia coli Mlc protein, accession number D90801, Smith-Waterman Score=1653.  
US-10-450-763-29558

Query Match 80.0%; Score 16.8; DB 9; Length 2250;  
Best Local Similarity 90.0%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGGCGG 20  
DB 663 GTAACGTCTGTAGTGGCGG 644

RESULT 37  
US-10-450-763-29562/c  
; Sequence 29562, Application US/10450763  
; Publication No. US20050196754A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 790CIP3/US  
; CURRENT APPLICATION NUMBER: US/10/450,763  
; PRIOR FILING DATE: 2003-06-11  
; PRIOR APPLICATION NUMBER: PCT/US01/08631  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
; SEQ ID NO 29562  
; LENGTH: 2830  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIMILAR  
; LOCATION: (1723)..(2307)  
; OTHER INFORMATION: 99% homologous to Escherichia coli RhsC protein precursor, accession number D90709, Smith-Waterman Score=1050.  
US-10-450-763-29562

Query Match 80.0%; Score 16.8; DB 9; Length 2830;  
Best Local Similarity 90.0%; Pred. No. 4.7e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGGCGG 20  
DB 1965 GTAACGTCTGTAGTGGCGG 1946

RESULT 38  
US-10-450-763-25465/c  
; Sequence 25465, Application US/10450763  
; Publication No. US20050196754A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 790CIP3/US  
; CURRENT APPLICATION NUMBER: US/10/450,763  
; PRIOR FILING DATE: 2003-06-11  
; PRIOR APPLICATION NUMBER: PCT/US01/08631  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
; SEQ ID NO 25465  
; LENGTH: 3039  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIMILAR  
; LOCATION: (2587)..(2988)  
; OTHER INFORMATION: 99% homologous to Escherichia coli rhsA, accession number X78541, Smith-Waterman Score=707.  
US-10-450-763-25465

Query Match 80.0%; Score 16.8; DB 9; Length 3039;  
Best Local Similarity 90.0%; Pred. No. 4.7e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGGCGG 20  
DB 2829 GTAACGTCTGTAGTGGCGG 2810

RESULT 39  
US-10-450-763-29044  
; Sequence 29044, Application US/10450763  
; Publication No. US20050196754A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 790CIP3/US  
; CURRENT APPLICATION NUMBER: US/10/450,763  
; PRIOR FILING DATE: 2003-06-11  
; PRIOR APPLICATION NUMBER: PCT/US01/08631  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
; SEQ ID NO 29044  
; LENGTH: 3039  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIMILAR  
; LOCATION: (453)..(52)  
; OTHER INFORMATION: 99% homologous to Escherichia coli rhsA, accession number X78541, Smith-Waterman Score=707.  
US-10-450-763-29044

Query Match 80.0%; Score 16.8; DB 9; Length 3039;

```
Best Local Similarity 90.0%; Pred. No. 4.7e+02; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 2;

Qy 1 GCAAGTGCTGTAGTGGCGG 20
    ||| ||||| ||||| |||||
Db 211 GTAACGTCTGTAGTGGCGG 230

RESULT 40
US-10-450-763-29143/c
; Sequence 29143, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 29143
; LENGTH: 3039
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (2587)..(2988)
; OTHER INFORMATION: 99% homologous to Escherichia coli rhsA, accession number
; OTHER INFORMATION: X78541, Smith-Waterman Score=707.
US-10-450-763-29143

Query Match 80.0%; Score 16.8; DB 9; Length 3039;
Best Local Similarity 90.0%; Pred. No. 4.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTGCTGTAGTGGCGG 20
    ||| ||||| ||||| |||||
Db 2829 GTAACGTCTGTAGTGGCGG 2810

RESULT 41
US-10-450-763-21560
; Sequence 21560, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 21560
; LENGTH: 3355
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (648)..(58)
; OTHER INFORMATION: 98% homologous to Escherichia coli RhsB core protein with
; OTHER INFORMATION: unique extension, accession number U00039, Smith-Waterman Score=104
```

```
US-10-450-763-21560

Query Match 80.0%; Score 16.8; DB 9; Length 3355;
Best Local Similarity 90.0%; Pred. No. 4.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTGCTGTAGTGGCGG 20
    ||| ||||| ||||| |||||
Db 457 GTAACGTCTGTAGTGGCGG 476

RESULT 42
US-09-815-242-6287/c
; Sequence 6287, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6287
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(4134)
US-09-815-242-6287

Query Match 80.0%; Score 16.8; DB 3; Length 4134;
Best Local Similarity 90.0%; Pred. No. 4.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTGCTGTAGTGGCGG 20
    ||| ||||| ||||| |||||
Db 243 GTAACGTCTGTAGTGGCGG 224

RESULT 43
US-10-287-274-296/c
; Sequence 296, Application US/10287274
; Publication No. US20030181408A1
; GENERAL INFORMATION:
; APPLICANT: Forsyth, R. Allyn
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERAPY
; FILE REFERENCE: ELITRA.008DV1
```

; CURRENT APPLICATION NUMBER: US/10/287,274  
; CURRENT FILING DATE: 2002-10-31  
; PRIOR APPLICATION NUMBER: US 60/164415  
; PRIOR FILING DATE: 1999-11-09  
; PRIOR APPLICATION NUMBER: US 09/711164  
; PRIOR FILING DATE: 2000-11-09  
; NUMBER OF SEQ ID NOS: 469  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 296  
; LENGTH: 4134  
; TYPE: DNA  
; ORGANISM: Escherichia coli  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(4134)  
US-10-287-274-296

Query Match 80.0%; Score 16.8; DB 6; Length 4134;  
Best Local Similarity 90.0%; Pred. No. 4.7e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 20  
||| ||||| ||||| |||||  
Db 243 GTAACGTGCTGTAGGTGCGGG 224

## RESULT 44

US-10-282-122A-6547/c  
; Sequence 6547, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 78614

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 6547

; LENGTH: 4134

; TYPE: DNA

; ORGANISM: Escherichia coli  
US-10-282-122A-6547

Query Match 80.0%; Score 16.8; DB 7; Length 4134;  
Best Local Similarity 90.0%; Pred. No. 4.7e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 20  
||| ||||| ||||| |||||  
Db 243 GTAACGTGCTGTAGGTGCGGG 224

## RESULT 45

US-10-282-122A-6875/c

; Sequence 6875, Application US/10282122A

; Publication No. US20040029129A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu

; APPLICANT: Zamudio, Carlos

; APPLICANT: Malone, Cheryl

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari

; APPLICANT: Zyskind, Judith

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John

; APPLICANT: Carr, Grant

; APPLICANT: Yamamoto, Robert

; APPLICANT: Forsyth, R.

; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 78614

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 6875

; LENGTH: 4194

; TYPE: DNA

; ORGANISM: Escherichia coli

US-10-282-122A-6875

Query Match 80.0%; Score 16.8; DB 7; Length 4194;  
Best Local Similarity 90.0%; Pred. No. 4.7e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 20  
||| ||||| ||||| |||||  
Db 243 GTAACGTGCTGTAGGTGCGGG 224

## RESULT 46

US-10-282-122A-6876/c

```
; Sequence 6876, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/257,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6876
; LENGTH: 4236
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-282-122A-6876

Query Match      80.0%; Score 16.8; DB 7; Length 4236;
Best Local Similarity 90.0%; Pred. No. 4.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCTGTAGTGCGGG 20
Db 243 GTAACGTCTGTAGTGCGGG 224

RESULT 47
US-10-450-763-26014/c
; Sequence 26014, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
```

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; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 26014
; LENGTH: 5471
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (1864)..(926)
; OTHER INFORMATION: 96% homologous to Escherichia coli K12 putative inner
; OTHER INFORMATION: membrane component for iron transport, accession number
; OTHER INFORMATION: AE000162, Smith-Waterman Score=1505.
US-10-450-763-26014

Query Match      80.0%; Score 16.8; DB 9; Length 5471;
Best Local Similarity 90.0%; Pred. No. 4.8e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCTGTAGTGCGGG 20
Db 4049 GTAACGTCTGTAGTGCGGG 4030

RESULT 48
US-10-114-170-226/c
; Sequence 226, Application US/10114170
; Publication No. US20030023075A1
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; Perna, Nicole T.
; Plunkett, Guy
; Welch, Rod
; TITLE OF INVENTION: No. US20030023075A1 Sequences of E. coli O157
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/114,170
; FILING DATE: 01-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/453,702
; FILING DATE: 03-DEC-1999
; APPLICATION NUMBER: 60/110,955
; FILING DATE: 04-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.95017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 226:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5519
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 226:
US-10-114-170-226
```

```
Query Match      80.0%; Score 16.8; DB 5; Length 5519;
Best Local Similarity 90.0%; Pred. No. 4.8e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGTGGG 20
Db 347 GTAACGTCTGTAGTGTGGG 328

RESULT 49
US-08-781-986A-45
; Sequence 45, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9072 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986A-45

Query Match      80.0%; Score 16.8; DB 2; Length 9072;
Best Local Similarity 90.0%; Pred. No. 4.8e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGTGGG 20
Db 2901 GCAAGTTATGTAGTGTGGG 2920

RESULT 50
US-10-329-624-45
; Sequence 45, Application US/10329624
; Publication No. US20040043037A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/329,624
; FILING DATE: 27-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/956,171
; FILING DATE: October 20, 1997
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9072 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-10-329-624-45

Query Match      80.0%; Score 16.8; DB 7; Length 9072;
Best Local Similarity 90.0%; Pred. No. 4.8e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGTGGG 20
Db 2901 GCAAGTTATGTAGTGTGGG 2920

Search completed: January 27, 2006, 07:20:39
Job time : 350.5 secs
```

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OM nucleic - nucleic search, using sw model

Run on: January 27, 2006, 05:44:44 ; Search time 396 Seconds  
(without alignments)  
44.051 Million cell updates/sec

Title: US-10-070-415A-1

Perfect score: 21

Sequence: 1 cccgtgaggaactwtgtct 21

Scoring table: IDENTITY NUC

Gapop 10\_0 , Gapext 1.0

Searched: 6059551 seqs, 41533918 residues

Total number of hits satisfying chosen parameters: 12119102

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications\_NA\_New.\*

1: /cgn2\_6/prodata/2/pubpna/US08\_NEW\_PUB.seq.\*  
2: /cgn2\_6/prodata/2/pubpna/US06\_NEW\_PUB.seq.\*  
3: /cgn2\_6/prodata/2/pubpna/US07\_NEW\_PUB.seq.\*  
4: /cgn2\_6/prodata/2/pubpna/PCT\_NEW\_PUB.seq.\*  
5: /cgn2\_6/prodata/2/pubpna/US09\_NEW\_PUB.seq.\*  
6: /cgn2\_6/prodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
7: /cgn2\_6/prodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
8: /cgn2\_6/prodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
9: /cgn2\_6/prodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
10: /cgn2\_6/prodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
11: /cgn2\_6/prodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20.6	98.1	7979	7	US-10-509-921-9
2	20.6	98.1	7979	7	US-10-509-921-10
3	20.6	98.1	7979	7	US-10-509-921-11
4	20.6	98.1	7979	7	US-10-509-921-12
5	20.6	98.1	7980	7	US-10-509-921-4
6	20.6	98.1	7980	7	US-10-509-921-5
7	20.6	98.1	7983	7	US-10-509-921-7
8	20.6	98.1	7989	7	US-10-509-921-2
9	20.6	98.1	7989	7	US-10-509-921-6
10	20.6	98.1	7989	7	US-10-509-921-8
11	20.6	98.1	7989	7	US-10-509-921-13
12	20.6	98.1	7989	7	US-10-509-921-14
13	20.6	98.1	7989	8	US-11-119-330-1
14	20.6	98.1	7992	8	US-10-509-921-3
15	20.6	98.1	7992	8	US-11-111-686-1
16	20.6	98.1	7992	8	US-11-111-686-2
17	20.6	98.1	7992	8	US-11-111-686-4
18	20.6	98.1	7992	8	US-11-111-686-5
19	20.6	98.1	7992	8	US-11-111-686-6
20	20.6	98.1	7995	8	US-11-111-686-3
21	20.6	98.1	9599	7	US-10-985-205-1
22	17	81.0	1094	7	US-10-750-185-51689

c	23	17	81.0	1094	7	US-10-750-623-51689	Sequence 51689, A
	24	17	81.0	3216	7	US-10-750-185-39720	Sequence 39720, A
	25	17	81.0	3216	7	US-10-750-623-39720	Sequence 39720, A
	26	16.4	78.1	1752	7	US-10-750-185-37350	Sequence 37350, A
	27	16.4	78.1	1752	7	US-10-750-623-37350	Sequence 37350, A
	28	15.8	75.2	509	8	US-11-020-772-32	Sequence 32, Appl
c	29	15.8	75.2	877	7	US-10-750-185-36885	Sequence 36885, A
c	30	15.8	75.2	877	7	US-10-750-623-36885	Sequence 36885, A
	31	15.8	75.2	2226	7	US-10-750-185-24847	Sequence 24847, A
	32	15.8	75.2	2226	7	US-10-750-623-24847	Sequence 24847, A
c	33	15.8	75.2	3338	7	US-10-750-185-26147	Sequence 26147, A
c	34	15.8	75.2	3338	7	US-10-750-623-26147	Sequence 26147, A
c	35	15.8	75.2	3534	7	US-10-750-185-36810	Sequence 36810, A
	36	15.8	75.2	3534	7	US-10-750-623-36810	Sequence 36810, A
	37	15.8	75.2	147700	7	US-10-857-780-3	Sequence 3, Appl
c	38	15.8	75.2	149419	8	US-11-112-908-49	Sequence 49, Appl
c	39	15.8	75.2	166111	8	US-11-112-908-47	Sequence 47, Appl
	40	15.4	73.3	600	7	US-10-750-185-460	Sequence 460, App
	41	15.4	73.3	600	7	US-10-750-623-460	Sequence 460, App
	42	15.4	73.3	670	7	US-10-750-185-61723	Sequence 61723, A
	43	15.4	73.3	670	7	US-10-750-623-61723	Sequence 61723, A
	44	15.4	73.3	1374	7	US-10-750-185-51706	Sequence 51706, A
	45	15.4	73.3	1374	7	US-10-750-623-51706	Sequence 51706, A
	46	15.4	73.3	1467	7	US-10-750-185-38999	Sequence 38999, A
	47	15.4	73.3	1467	7	US-10-750-623-38999	Sequence 38999, A
c	48	15.4	73.3	1493	8	US-11-136-527-2274	Sequence 2274, Ap
c	49	15.4	73.3	3443	8	US-11-136-527-3734	Sequence 3734, Ap
c	50	15.4	73.3	5506	7	US-10-821-234-277	Sequence 277, App
c	51	15.4	73.3	5510	8	US-11-150-406-1	Sequence 1, Appl
	52	15.2	72.4	25	8	US-11-121-849-409578	Sequence 409578, A
c	53	15.2	72.4	201	7	US-10-995-561-28272	Sequence 28272, A
	54	15.2	72.4	201	7	US-10-995-561-61097	Sequence 61097, A
c	55	15.2	72.4	786	7	US-10-750-185-32024	Sequence 32024, A
c	56	15.2	72.4	786	7	US-10-750-623-32024	Sequence 32024, A
c	57	15.2	72.4	813	7	US-10-750-185-53254	Sequence 53254, A
c	58	15.2	72.4	88116	7	US-10-750-623-53254	Sequence 53254, A
c	59	15.2	72.4	88116	7	US-10-995-561-13351	Sequence 13351, A
c	60	15.2	72.4	222094	7	US-10-995-561-13244	Sequence 13244, A
	61	15	71.4	25	8	US-11-121-849-311219	Sequence 311219, A
c	62	15	71.4	876	7	US-10-750-185-48349	Sequence 48349, A
c	63	15	71.4	876	7	US-10-750-623-48349	Sequence 48349, A
c	64	15	71.4	1432	7	US-10-750-185-51771	Sequence 51771, A
c	65	15	71.4	1432	7	US-10-750-623-51771	Sequence 51771, A
c	66	15	71.4	1783	7	US-10-750-185-48464	Sequence 48464, A
c	67	15	71.4	1783	7	US-10-750-623-48464	Sequence 48464, A
c	68	15	71.4	189539	8	US-11-121-086-15	Sequence 16, Appl
c	69	14.8	70.5	19	9	US-11-101-244-1059418	Sequence 1059418, A
c	70	14.8	70.5	19	10	US-11-083-784-1059418	Sequence 1059418, A
c	71	14.8	70.5	25	8	US-11-121-849-536730	Sequence 536730, A
	72	14.8	70.5	25	8	US-10-310-914A-18319	Sequence 18319, A
	73	14.8	70.5	201	7	US-10-995-561-31062	Sequence 31062, A
c	74	14.8	70.5	201	8	US-11-124-368A-20547	Sequence 20547, A
c	75	14.8	70.5	201	8	US-11-124-368A-20939	Sequence 20939, A
c	76	14.8	70.5	201	8	US-11-124-368A-21039	Sequence 21039, A
c	77	14.8	70.5	575	8	US-11-000-688-1285	Sequence 1285, Ap
c	78	14.8	70.5	720	8	US-11-118-855-3	Sequence 3, Appl
c	79	14.8	70.5	1947	7	US-10-750-185-49960	Sequence 49960, A
c	80	14.8	70.5	1947	7	US-10-750-623-49960	Sequence 49960, A
c	81	14.8	70.5	2251	7	US-10-750-185-60956	Sequence 60956, A
c	82	14.8	70.5	2251	7	US-10-750-623-60956	Sequence 60956, A
c	83	14.8	70.5	2454	8	US-11-000-688-1287	Sequence 1287, Ap
	84	14.8	70.5	2462	8	US-11-136-527-264	Sequence 264, App
	85	14.8	70.5	2879	8	US-11-124-368A-166	Sequence 166, App
c	86	14.8	70.5	3260	8	US-11-136-527-2356	Sequence 2356, Ap
c	87	14.8	70.5	3583	8	US-11-136-527-15	Sequence 15, App
c	88	14.8	70.5	15660	7	US-10-453-372-1001	Sequence 1001, Ap
c	89	14.8	70.5	18755	8	US-11-124-368A-2937	Sequence 2937, Ap
c	90	14.8	70.5	41081	8	US-11-124-368A-2931	Sequence 2931, Ap
	91	14.8	70.5	65723	7	US-10-995-561-13200	Sequence 13200, A
	92	14.8	70.5	100387	8	US-11-121-086-94	Sequence 94, Appl
	93	14.8	70.5	103660	7	US-10-995-561-13253	Sequence 13253, A
c	94	14.8	70.5	136284	7	US-10-775-169-149	Sequence 149, App
c	95	14.8	70.5	212716	8	US-11-121-086-95	Sequence 95, Appl

C 96 14.8 70.5 214000 7 US-10-769-744-1 Sequence 1, Appli  
C 97 14.8 70.5 246960 8 US-11-121-086-8 Sequence 8, Appli  
C 98 14.8 70.5 1080000 7 US-10-928-446A-1 Sequence 1, Appli  
C 99 14.8 70.5 1080000 7 US-10-928-446A-181 Sequence 181, App  
C 100 14.8 70.5 1080000 7 US-10-928-446A-183 Sequence 183, App

## ALIGNMENTS

## RESULT 1

US-10-509-921-9  
; Sequence 9, Application US/10509921  
; Publication No. US20050250093A1  
; GENERAL INFORMATION:  
; APPLICANT: SmithKline Beecham Corporation  
; TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons  
; FILE REFERENCE: P51335  
; CURRENT APPLICATION NUMBER: US/10/509,921  
; CURRENT FILING DATE: 2004-10-01  
; PRIOR APPLICATION NUMBER: 60/369,685  
; PRIOR FILING DATE: 2002-04-03  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 7979  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Thepolynucleotide sequence encodes sequences from  
; OTHER INFORMATION: HCV J4(B/R1) Replicons  
US-10-509-921-9

Query Match 98.1%; Score 20.6; DB 7; Length 7979;  
Best Local Similarity 95.2%; Pred. No. 0.44;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21  
|||||  
Db 43 CCTGTGAGGAAGTCTGTCT 63

## RESULT 2

US-10-509-921-10  
; Sequence 10, Application US/10509921  
; Publication No. US20050250093A1  
; GENERAL INFORMATION:  
; APPLICANT: SmithKline Beecham Corporation  
; TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons  
; FILE REFERENCE: P51335  
; CURRENT APPLICATION NUMBER: US/10/509,921  
; CURRENT FILING DATE: 2004-10-01  
; PRIOR APPLICATION NUMBER: 60/369,685  
; PRIOR FILING DATE: 2002-04-03  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 7979  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Thepolynucleotide sequence encodes sequences from  
; OTHER INFORMATION: HCV J4(B/R1(C))Replicons  
US-10-509-921-10

Query Match 98.1%; Score 20.6; DB 7; Length 7979;  
Best Local Similarity 95.2%; Pred. No. 0.44;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21  
|||||  
Db 43 CCTGTGAGGAAGTCTGTCT 63

## RESULT 3

US-10-509-921-11  
; Sequence 11, Application US/10509921  
; Publication No. US20050250093A1  
; GENERAL INFORMATION:  
; APPLICANT: SmithKline Beecham Corporation  
; TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons  
; FILE REFERENCE: P51335  
; CURRENT APPLICATION NUMBER: US/10/509,921  
; CURRENT FILING DATE: 2004-10-01  
; PRIOR APPLICATION NUMBER: 60/369,685  
; PRIOR FILING DATE: 2002-04-03  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 7979  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Thepolynucleotide sequence encodes sequences from  
; OTHER INFORMATION: HCV J4 Replicons  
US-10-509-921-11

Query Match 98.1%; Score 20.6; DB 7; Length 7979;  
Best Local Similarity 95.2%; Pred. No. 0.44;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21  
|||||  
Db 43 CCTGTGAGGAAGTCTGTCT 63

## RESULT 4

US-10-509-921-12  
; Sequence 12, Application US/10509921  
; Publication No. US20050250093A1  
; GENERAL INFORMATION:  
; APPLICANT: SmithKline Beecham Corporation  
; TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons  
; FILE REFERENCE: P51335  
; CURRENT APPLICATION NUMBER: US/10/509,921  
; CURRENT FILING DATE: 2004-10-01  
; PRIOR APPLICATION NUMBER: 60/369,685  
; PRIOR FILING DATE: 2002-04-03  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 7979  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Thepolynucleotide sequence encodes sequences from  
; OTHER INFORMATION: HCV J4 Replicons  
US-10-509-921-12

Query Match 98.1%; Score 20.6; DB 7; Length 7979;  
Best Local Similarity 95.2%; Pred. No. 0.44;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21  
|||||  
Db 43 CCTGTGAGGAAGTCTGTCT 63

## RESULT 5

US-10-509-921-4  
; Sequence 4, Application US/10509921  
; Publication No. US20050250093A1  
; GENERAL INFORMATION:  
; APPLICANT: SmithKline Beecham Corporation  
; TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons  
; FILE REFERENCE: P51335



0

Qy 1 CCCTGTGAGGAAGTCTGTCT 21  
Db 43 CCCTGTGAGGAAGTCTGTCT 63

RESULT 10  
US-10-509-921-8  
; Sequence 8, Application US/10509921  
; Publication No. US20050250093A1  
; GENERAL INFORMATION:  
; APPLICANT: SmithKline Beecham Corporation  
; TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons  
; FILE REFERENCE: P51335  
; CURRENT APPLICATION NUMBER: US/10/509,921  
; CURRENT FILING DATE: 2004-10-01  
; PRIOR APPLICATION NUMBER: 60/369,685  
; PRIOR FILING DATE: 2002-04-03  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 7989  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Thepolynucleotide sequence encodes sequences from  
; OTHER INFORMATION: HCV J4(J4 M/S)Replicons  
US-10-509-921-8

Query Match 98.1%; Score 20.6; DB 7; Length 7989;  
Best Local Similarity 95.2%; Pred. No. 0.44;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAAGTCTGTCT 21  
Db 43 CCCTGTGAGGAAGTCTGTCT 63

RESULT 11  
US-10-509-921-13  
; Sequence 13, Application US/10509921  
; Publication No. US20050250093A1  
; GENERAL INFORMATION:  
; APPLICANT: SmithKline Beecham Corporation  
; TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons  
; FILE REFERENCE: P51335  
; CURRENT APPLICATION NUMBER: US/10/509,921  
; CURRENT FILING DATE: 2004-10-01  
; PRIOR APPLICATION NUMBER: 60/369,685  
; PRIOR FILING DATE: 2002-04-03  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 7989  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Thepolynucleotide sequence encodes sequences from  
; OTHER INFORMATION: HCV J4(BB7/J4NS5B)Replicons  
US-10-509-921-13

Query Match 98.1%; Score 20.6; DB 7; Length 7989;  
Best Local Similarity 95.2%; Pred. No. 0.44;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAAGTCTGTCT 21  
Db 43 CCCTGTGAGGAAGTCTGTCT 63

RESULT 12  
US-10-509-921-14  
; Sequence 14, Application US/10509921

; Publication No. US20050250093A1  
; GENERAL INFORMATION:  
; APPLICANT: SmithKline Beecham Corporation  
; TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons  
; FILE REFERENCE: P51335  
; CURRENT APPLICATION NUMBER: US/10/509,921  
; CURRENT FILING DATE: 2004-10-01  
; PRIOR APPLICATION NUMBER: 60/369,685  
; PRIOR FILING DATE: 2002-04-03  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 7989  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Thepolynucleotide sequence encodes sequences from  
; OTHER INFORMATION: HCV H77(pBB7-SN)Replicons  
US-10-509-921-14

Query Match 98.1%; Score 20.6; DB 7; Length 7989;  
Best Local Similarity 95.2%; Pred. No. 0.44;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAAGTCTGTCT 21  
Db 43 CCCTGTGAGGAAGTCTGTCT 63

RESULT 13  
US-11-119-330-1  
; Sequence 1, Application US/11119330  
; Publication No. US20050260568A1  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Min  
; APPLICANT: Lemm, Julie A.  
; APPLICANT: O'Boyle, Donald R.  
; APPLICANT: Nower, Peter  
; TITLE OF INVENTION: HEPATITIS C VIRUS ASSAYS  
; FILE REFERENCE: 10283 NP  
; CURRENT APPLICATION NUMBER: US/11/119,330  
; CURRENT FILING DATE: 2005-04-29  
; PRIOR APPLICATION NUMBER: 60/567,270  
; PRIOR FILING DATE: 2004-04-30  
; PRIOR APPLICATION NUMBER: 60/568,590  
; PRIOR FILING DATE: 2004-05-06  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1  
; LENGTH: 7989  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HCV Replicon  
US-11-119-330-1

Query Match 98.1%; Score 20.6; DB 8; Length 7989;  
Best Local Similarity 95.2%; Pred. No. 0.44;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAAGTCTGTCT 21  
Db 43 CCCTGTGAGGAAGTCTGTCT 63

RESULT 14  
US-10-509-921-3  
; Sequence 3, Application US/10509921  
; Publication No. US20050250093A1  
; GENERAL INFORMATION:  
; APPLICANT: SmithKline Beecham Corporation  
; TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons  
; FILE REFERENCE: P51335

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; CURRENT APPLICATION NUMBER: US/10/509,921
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/369,685
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 7992
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Thepolynucleotide sequence encodes sequences from
; OTHER INFORMATION: HCV H77(BB7-Fl/P2) Replicons
US-10-509-921-3

Query Match          98.1%; Score 20.6; DB 7; Length 7992;
Best Local Similarity 95.2%; Pred. No. 0.44;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
DB 43 CCCTGTGAGGAAGTCTGTCT 63

RESULT 15
US-11-111-686-1
; Sequence 1, Application US/11111686
; Publication No. US20050260221A1
; GENERAL INFORMATION:
; APPLICANT: ANADYS Pharmaceuticals, Inc.
; APPLICANT: Bichko, Vadim
; TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY REP
; FILE REFERENCE: 0342/1H395US1
; CURRENT APPLICATION NUMBER: US/11/111,686
; CURRENT FILING DATE: 2005-04-20
; PRIOR APPLICATION NUMBER: US/10/005,469
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US 60/245,866
; PRIOR FILING DATE: 2000-11-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 7992
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCV replicon I377/NS3-3'UTR
US-11-111-686-1

Query Match          98.1%; Score 20.6; DB 8; Length 7992;
Best Local Similarity 95.2%; Pred. No. 0.44;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
DB 43 CCCTGTGAGGAAGTCTGTCT 63

RESULT 16
US-11-111-686-2
; Sequence 2, Application US/11111686
; Publication No. US20050260221A1
; GENERAL INFORMATION:
; APPLICANT: ANADYS Pharmaceuticals, Inc.
; APPLICANT: Bichko, Vadim
; TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY REP
; FILE REFERENCE: 0342/1H395US1
; CURRENT APPLICATION NUMBER: US/11/111,686
; CURRENT FILING DATE: 2005-04-20
; PRIOR APPLICATION NUMBER: US/10/005,469
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US 60/245,866
; PRIOR FILING DATE: 2000-11-07

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```

; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 7992
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCV Replicon RNA from cell line HCVR2
US-11-111-686-2

Query Match          98.1%; Score 20.6; DB 8; Length 7992;
Best Local Similarity 95.2%; Pred. No. 0.44;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
DB 43 CCCTGTGAGGAAGTCTGTCT 63

RESULT 17
US-11-111-686-4
; Sequence 4, Application US/11111686
; Publication No. US20050260221A1
; GENERAL INFORMATION:
; APPLICANT: ANADYS Pharmaceuticals, Inc.
; APPLICANT: Bichko, Vadim
; TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY R
; FILE REFERENCE: 0342/1H395US1
; CURRENT APPLICATION NUMBER: US/11/111,686
; CURRENT FILING DATE: 2005-04-20
; PRIOR APPLICATION NUMBER: US/10/005,469
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US 60/245,866
; PRIOR FILING DATE: 2000-11-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 7992
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCV Replicon RNA from cell line HCVR9
US-11-111-686-4

Query Match          98.1%; Score 20.6; DB 8; Length 7992;
Best Local Similarity 95.2%; Pred. No. 0.44;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
DB 43 CCCTGTGAGGAAGTCTGTCT 63

RESULT 18
US-11-111-686-5
; Sequence 5, Application US/11111686
; Publication No. US20050260221A1
; GENERAL INFORMATION:
; APPLICANT: ANADYS Pharmaceuticals, Inc.
; APPLICANT: Bichko, Vadim
; TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY R
; FILE REFERENCE: 0342/1H395US1
; CURRENT APPLICATION NUMBER: US/11/111,686
; CURRENT FILING DATE: 2005-04-20
; PRIOR APPLICATION NUMBER: US/10/005,469
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US 60/245,866
; PRIOR FILING DATE: 2000-11-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 7992
; TYPE: DNA

```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCV Replicon from cell line HCVR22
US-11-111-686-5

Query Match      98.1%; Score 20.6; DB 8; Length 7992;
Best Local Similarity 95.2%; Pred. No. 0.44;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
Db 43 CCTGTGAGGAAGTCTGTCT 63

RESULT 19
US-11-111-686-6
; Sequence 6, Application US/11111686
; Publication No. US20050260221A1
; GENERAL INFORMATION:
; APPLICANT: Anadys Pharmaceuticals, Inc.
; APPLICANT: Bichko, Vadim
; TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY RE
; FILE REFERENCE: 0342/1H395US1
; CURRENT APPLICATION NUMBER: US/11/111,686
; CURRENT FILING DATE: 2005-04-20
; PRIOR APPLICATION NUMBER: US/10/005,469
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US 60/245,866
; PRIOR FILING DATE: 2000-11-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 7992
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCV Replicon from cell line HCVR24
US-11-111-686-6

Query Match      98.1%; Score 20.6; DB 8; Length 7992;
Best Local Similarity 95.2%; Pred. No. 0.44;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
Db 43 CCTGTGAGGAAGTCTGTCT 63

RESULT 20
US-11-111-686-3
; Sequence 3, Application US/11111686
; Publication No. US20050260221A1
; GENERAL INFORMATION:
; APPLICANT: Anadys Pharmaceuticals, Inc.
; APPLICANT: Bichko, Vadim
; TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY RE
; FILE REFERENCE: 0342/1H395US1
; CURRENT APPLICATION NUMBER: US/11/111,686
; CURRENT FILING DATE: 2005-04-20
; PRIOR APPLICATION NUMBER: US/10/005,469
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US 60/245,866
; PRIOR FILING DATE: 2000-11-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 7995
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCV Replicon RNA from cell line HCVR8
US-11-111-686-3

```

```

Query Match      98.1%; Score 20.6; DB 8; Length 7995;
Best Local Similarity 95.2%; Pred. No. 0.44;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
Db 43 CCTGTGAGGAAGTCTGTCT 63

RESULT 21
US-10-985-205-1
; Sequence 1, Application US/10985205
; Publication No. US20050266400A1
; GENERAL INFORMATION:
; APPLICANT: Dumonceaux, Julie
; APPLICANT: Cormier, Emmanuel G.
; APPLICANT: Gardner, Jason P.
; APPLICANT: Dragic, Tatjana
; TITLE OF INVENTION: NOVEL SEQUENCES ENCODING HEPATITIS C VIRUS GLYCOPROTEINS
; FILE REFERENCE: 71242-A/JPW/AJD
; CURRENT APPLICATION NUMBER: US/10/985,205
; CURRENT FILING DATE: 2004-11-09
; PRIOR APPLICATION NUMBER: US 60/519,536
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 9599
; TYPE: DNA
; ORGANISM: Hepatitis C virus
; OTHER INFORMATION:
US-10-985-205-1

Query Match      98.1%; Score 20.6; DB 7; Length 9599;
Best Local Similarity 95.2%; Pred. No. 0.45;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
Db 43 CCTGTGAGGAAGTCTGTCT 63

RESULT 22
US-10-750-185-51689/c
; Sequence 51689, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: Denise, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MW1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51689
; LENGTH: 1094
; TYPE: DNA
; ORGANISM: Bovine
; OTHER INFORMATION:
US-10-750-185-51689

Query Match      81.0%; Score 17; DB 7; Length 1094;
Best Local Similarity 89.5%; Pred. No. 23;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 19

```

Db 144 CCTGTGAGGAACCTTCTAT 126

## RESULT 23

US-10-750-623-51689/c  
; Sequence 51689, Application US/10750623  
; Publication No. US20050287531A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-1  
; CURRENT APPLICATION NUMBER: US/10/750,623  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIN version 3.1  
; SEQ ID NO 51689  
; LENGTH: 1094  
; TYPE: DNA  
; ORGANISM: Bovine 19866880406659  
US-10-750-623-51689

Query Match 81.0%; Score 17; DB 7; Length 1094;  
Best Local Similarity 89.5%; Pred. No. 23;  
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAACCTTCTGT 19  
|||||  
Db 144 CCTGTGAGGAACCTTCTAT 126

## RESULT 24

US-10-750-185-39720  
; Sequence 39720, Application US/10750185  
; Publication No. US20050260603A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-2  
; CURRENT APPLICATION NUMBER: US/10/750,185  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIN version 3.1  
; SEQ ID NO 39720  
; LENGTH: 3216  
; TYPE: DNA  
; ORGANISM: Bovine 19866881421275  
US-10-750-185-39720

Query Match 81.0%; Score 17; DB 7; Length 3216;  
Best Local Similarity 89.5%; Pred. No. 27;  
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAACCTTCTGT 19  
|||||  
Db 2155 CCTTTGAGGAACCTTCTGT 2173

## RESULT 25

US-10-750-623-39720  
; Sequence 39720, Application US/10750623  
; Publication No. US20050287531A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-1  
; CURRENT APPLICATION NUMBER: US/10/750,623  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIN version 3.1  
; SEQ ID NO 39720  
; LENGTH: 3216  
; TYPE: DNA  
; ORGANISM: Bovine 19866881421275  
US-10-750-623-39720

Query Match 81.0%; Score 17; DB 7; Length 3216;  
Best Local Similarity 89.5%; Pred. No. 27;  
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAACCTTCTGT 19  
|||||  
Db 2155 CCTTTGAGGAACCTTCTGT 2173

## RESULT 26

US-10-750-185-37350  
; Sequence 37350, Application US/10750185  
; Publication No. US20050260603A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-2  
; CURRENT APPLICATION NUMBER: US/10/750,185  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIN version 3.1  
; SEQ ID NO 37350  
; LENGTH: 1752  
; TYPE: DNA  
; ORGANISM: Bovine 19866880501591  
US-10-750-185-37350

Query Match 78.1%; Score 16.4; DB 7; Length 1752;  
Best Local Similarity 85.0%; Pred. No. 51;  
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAACCTTCTGT 20  
|||||  
Db 665 CCTTTGAGGAACCTTCTGT 684

## RESULT 27

US-10-750-623-37350  
; Sequence 37350, Application US/10750623

```
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 37350
; LENGTH: 1752
; TYPE: DNA
; ORGANISM: Bovine 19866880501591
US-10-750-623-37350

Query Match      78.1%; Score 16.4; DB 7; Length 1752;
Best Local Similarity 85.0%; Pred. No. 51;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGCTC 20
Db 665 CCTTGTGAGGAGCTTCTGTC 684

RESULT 28
US-11-020-772-32
; Publication 32, Application US/11020772
; Publication No. US20050256043A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig, Linda B.
; TITLE OF INVENTION: HIV Antisense Proteins
; FILE REFERENCE: 25125, 0001
; CURRENT APPLICATION NUMBER: US/11/020,772
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: US 09/249,542
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,640
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 08/853,703
; PRIOR FILING DATE: 1997-05-09
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 32
; LENGTH: 509
; TYPE: RNA
; ORGANISM: human immunodeficiency virus
; FEATURE:
; OTHER INFORMATION: HIV antisense HAP gene (clade A)
US-11-020-772-32

Query Match      75.2%; Score 15.8; DB 8; Length 509;
Best Local Similarity 52.4%; Pred. No. 86;
Matches 11; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGCTC 21
Db 128 CCCUGUCAGCAUCUCUGU 148

RESULT 29
US-10-750-185-36885/c
; Sequence 36885, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
```

```
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 36885
; LENGTH: 877
; TYPE: DNA
; ORGANISM: Bovine 19866880749700
US-10-750-185-36885

Query Match      75.2%; Score 15.8; DB 7; Length 877;
Best Local Similarity 81.0%; Pred. No. 93;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGCTC 21
Db 37 CCCTGTGAGGACCCACTGGCT 17

RESULT 30
US-10-750-623-36885/c
; Sequence 36885, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 36885
; LENGTH: 877
; TYPE: DNA
; ORGANISM: Bovine 19866880749700
US-10-750-623-36885

Query Match      75.2%; Score 15.8; DB 7; Length 877;
Best Local Similarity 81.0%; Pred. No. 93;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGCTC 21
Db 37 CCCTGTGAGGACCCACTGGCT 17

RESULT 31
US-10-750-185-24847
; Sequence 24847, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
```

; APPLICANT: BATES, Stephen  
 ; APPLICANT: FANTIN, Dennis  
 ; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
 ; FILE REFERENCE: MM1100-2  
 ; CURRENT APPLICATION NUMBER: US/10/750,185  
 ; CURRENT FILING DATE: 2003-12-31  
 ; PRIOR APPLICATION NUMBER: US 60/437,482  
 ; PRIOR FILING DATE: 2002-12-31  
 ; NUMBER OF SEQ ID NOS: 64922  
 ; SOFTWARE: PatentIN version 3.1  
 ; SEQ ID NO 24847  
 ; LENGTH: 2226  
 ; TYPE: DNA  
 ; ORGANISM: Bovine 19866880668698  
 US-10-750-185-24847

Query Match 75.2%; Score 15.8; DB 7; Length 2226;  
 Best Local Similarity 89.5%; Pred. No. 1.1e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGT 19  
 |||||  
 Db 937 CCCTGTGAGGAAGTCTGT 955

RESULT 32  
 US-10-750-623-24847  
 ; Sequence 24847, Application US/10750623  
 ; Publication No. US20050287531A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MMI GENOMICS, INC.  
 ; APPLICANT: DENISE, Sue K.  
 ; APPLICANT: KERR, Richard  
 ; APPLICANT: ROSENFELD, David  
 ; APPLICANT: HOLM, Tom  
 ; APPLICANT: BATES, Stephen  
 ; APPLICANT: FANTIN, Dennis  
 ; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
 ; FILE REFERENCE: MM1100-1  
 ; CURRENT APPLICATION NUMBER: US/10/750,623  
 ; CURRENT FILING DATE: 2003-12-31  
 ; PRIOR APPLICATION NUMBER: US 60/437,482  
 ; PRIOR FILING DATE: 2002-12-31  
 ; NUMBER OF SEQ ID NOS: 64922  
 ; SOFTWARE: PatentIN version 3.1  
 ; SEQ ID NO 24847  
 ; LENGTH: 2226  
 ; TYPE: DNA  
 ; ORGANISM: Bovine 19866880668698  
 US-10-750-623-24847

Query Match 75.2%; Score 15.8; DB 7; Length 2226;  
 Best Local Similarity 89.5%; Pred. No. 1.1e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGT 19  
 |||||  
 Db 937 CCCTGTGAGGAAGTCTGT 955

RESULT 33  
 US-10-750-185-26147/c  
 ; Sequence 26147, Application US/10750185  
 ; Publication No. US20050260603A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MMI GENOMICS, INC.  
 ; APPLICANT: DENISE, Sue K.  
 ; APPLICANT: KERR, Richard  
 ; APPLICANT: ROSENFELD, David  
 ; APPLICANT: HOLM, Tom  
 ; APPLICANT: BATES, Stephen  
 ; APPLICANT: FANTIN, Dennis  
 ; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

; FILE REFERENCE: MM1100-2  
 ; CURRENT APPLICATION NUMBER: US/10/750,185  
 ; CURRENT FILING DATE: 2003-12-31  
 ; PRIOR APPLICATION NUMBER: US 60/437,482  
 ; PRIOR FILING DATE: 2002-12-31  
 ; NUMBER OF SEQ ID NOS: 64922  
 ; SOFTWARE: PatentIN version 3.1  
 ; SEQ ID NO 26147  
 ; LENGTH: 3338  
 ; TYPE: DNA  
 ; ORGANISM: Bovine 19866881385217  
 US-10-750-185-26147

Query Match 75.2%; Score 15.8; DB 7; Length 3338;  
 Best Local Similarity 81.0%; Pred. No. 1.1e+02;  
 Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21  
 |||||  
 Db 911 CCAGTGGGAAGTCTGTCT 891

RESULT 34  
 US-10-750-623-26147/c  
 ; Sequence 26147, Application US/10750623  
 ; Publication No. US20050287531A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MMI GENOMICS, INC.  
 ; APPLICANT: DENISE, Sue K.  
 ; APPLICANT: KERR, Richard  
 ; APPLICANT: ROSENFELD, David  
 ; APPLICANT: HOLM, Tom  
 ; APPLICANT: BATES, Stephen  
 ; APPLICANT: FANTIN, Dennis  
 ; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
 ; FILE REFERENCE: MM1100-1  
 ; CURRENT APPLICATION NUMBER: US/10/750,623  
 ; CURRENT FILING DATE: 2003-12-31  
 ; PRIOR APPLICATION NUMBER: US 60/437,482  
 ; PRIOR FILING DATE: 2002-12-31  
 ; NUMBER OF SEQ ID NOS: 64922  
 ; SOFTWARE: PatentIN version 3.1  
 ; SEQ ID NO 26147  
 ; LENGTH: 3338  
 ; TYPE: DNA  
 ; ORGANISM: Bovine 19866881385217  
 US-10-750-623-26147

Query Match 75.2%; Score 15.8; DB 7; Length 3338;  
 Best Local Similarity 81.0%; Pred. No. 1.1e+02;  
 Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21  
 |||||  
 Db 911 CCAGTGGGAAGTCTGTCT 891

RESULT 35  
 US-10-750-185-36810/c  
 ; Sequence 36810, Application US/10750185  
 ; Publication No. US20050260603A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MMI GENOMICS, INC.  
 ; APPLICANT: DENISE, Sue K.  
 ; APPLICANT: KERR, Richard  
 ; APPLICANT: ROSENFELD, David  
 ; APPLICANT: HOLM, Tom  
 ; APPLICANT: BATES, Stephen  
 ; APPLICANT: FANTIN, Dennis  
 ; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
 ; FILE REFERENCE: MM1100-2  
 ; CURRENT APPLICATION NUMBER: US/10/750,185  
 ; CURRENT FILING DATE: 2003-12-31

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; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36810
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: Bovine 19866880404939
US-10-750-185-36810

Query Match          75.2%; Score 15.8; DB 7; Length 3534;
Best Local Similarity 81.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGAACTWCTGTCT 21
   |||||
Db 1802 CTCTGTGAGGAAGAACTAATGCCT 1782

RESULT 36
US-10-750-623-36810/c
; Sequence 36810, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36810
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: Bovine 19866880404939
US-10-750-623-36810

Query Match          75.2%; Score 15.8; DB 7; Length 3534;
Best Local Similarity 81.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGAACTWCTGTCT 21
   |||||
Db 1802 CTCTGTGAGGAAGAACTAATGCCT 1782

RESULT 37
US-10-857-780-3
; Sequence 3, Application US/10857780
; Publication No. US20050272043A1
; GENERAL INFORMATION:
; APPLICANT: ROTH, RICHARD B.
; APPLICANT: BRAUN, ANDREAS
; APPLICANT: KAMMERER, STEFAN M.
; APPLICANT: NELSON, MATTHEW ROBERTS
; APPLICANT: RENELAND, RIKARD HENRY
; APPLICANT: HOVAL-WRIGHTSON, CAROLYN R.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
; FILE REFERENCE: SEQ-4069-CP
; CURRENT APPLICATION NUMBER: US/10/857,780
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 10/723,681
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/490,234
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; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: 60/525,239
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 4962
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 147700
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (51510)..(51510)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (51526)..(51526)
; OTHER INFORMATION: n is a, c, g, or t
US-10-857-780-3

Query Match          75.2%; Score 15.8; DB 7; Length 147700;
Best Local Similarity 81.0%; Pred. No. 2e+02;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGAACTWCTGTCT 21
   |||||
Db 121582 CCTGTGAGGAAGAACTTCTTCT 121602

RESULT 38
US-11-112-908-49/c
; Sequence 49, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 49
; LENGTH: 149419
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-49

Query Match          75.2%; Score 15.8; DB 8; Length 149419;
Best Local Similarity 81.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGAACTWCTGTCT 21
   |||||
Db 117999 CCTGTGAGGAAGAACTTCTGTCT 117979

RESULT 39
US-11-112-908-47/c
; Sequence 47, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
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; CURRENT APPLICATION NUMBER: US/11/112,908  
 ; CURRENT FILING DATE: 2005-04-22  
 ; PRIOR APPLICATION NUMBER: US 60/564,758  
 ; PRIOR FILING DATE: 2004-04-23  
 ; PRIOR APPLICATION NUMBER: US 60/575,978  
 ; PRIOR FILING DATE: 2004-06-01  
 ; PRIOR APPLICATION NUMBER: US 60/631,702  
 ; PRIOR FILING DATE: 2004-11-30  
 ; PRIOR APPLICATION NUMBER: US 60/633,826  
 ; PRIOR FILING DATE: 2004-12-07  
 ; NUMBER OF SEQ ID NOS: 511  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 47  
 ; LENGTH: 166111  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-11-112-908-47

Query Match 75.2%; Score 15.8; DB 8; Length 166111;  
 Best Local Similarity 81.0%; Pred. No. 2.1e+02;  
 Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAACTWCTGTCT 21  
 DB 95099 CCTGTGAGGAACTWCTGTCT 95079

RESULT 40  
 US-10-750-185-460  
 ; Sequence 460, Application US/10750185  
 ; Publication No. US20050260603A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MMI GENOMICS, INC.  
 ; APPLICANT: DENISE, Sue K.  
 ; APPLICANT: KERR, Richard  
 ; APPLICANT: ROSENFELD, David  
 ; APPLICANT: HOLM, Tom  
 ; APPLICANT: BATES, Stephen  
 ; APPLICANT: FANTIN, Dennis  
 ; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
 ; FILE REFERENCE: MM1100-2  
 ; CURRENT APPLICATION NUMBER: US/10/750,185  
 ; CURRENT FILING DATE: 2003-12-31  
 ; PRIOR APPLICATION NUMBER: US 60/437,482  
 ; PRIOR FILING DATE: 2002-12-31  
 ; NUMBER OF SEQ ID NOS: 64922  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 460  
 ; LENGTH: 600  
 ; TYPE: DNA  
 ; ORGANISM: Bovine MMBT08269  
 US-10-750-185-460

Query Match 73.3%; Score 15.4; DB 7; Length 600;  
 Best Local Similarity 84.2%; Pred. No. 1.4e+02;  
 Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAACTWCTGTCT 19  
 DB 20 CCTGTGAGGAACTWCTGTCT 38

RESULT 41  
 US-10-750-623-460  
 ; Sequence 460, Application US/10750623  
 ; Publication No. US20050287531A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MMI GENOMICS, INC.  
 ; APPLICANT: DENISE, Sue K.  
 ; APPLICANT: KERR, Richard  
 ; APPLICANT: ROSENFELD, David  
 ; APPLICANT: HOLM, Tom  
 ; APPLICANT: BATES, Stephen

; APPLICANT: FANTIN, Dennis  
 ; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
 ; FILE REFERENCE: MM1100-1  
 ; CURRENT APPLICATION NUMBER: US/10/750,623  
 ; CURRENT FILING DATE: 2003-12-31  
 ; PRIOR APPLICATION NUMBER: US 60/437,482  
 ; PRIOR FILING DATE: 2002-12-31  
 ; NUMBER OF SEQ ID NOS: 64922  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 460  
 ; LENGTH: 600  
 ; TYPE: DNA  
 ; ORGANISM: Bovine MMBT08269  
 US-10-750-623-460

Query Match 73.3%; Score 15.4; DB 7; Length 600;  
 Best Local Similarity 84.2%; Pred. No. 1.4e+02;  
 Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAACTWCTGTCT 19  
 DB 20 CCTGTGAGGAACTWCTGTCT 38

RESULT 42  
 US-10-750-185-61723  
 ; Sequence 61723, Application US/10750185  
 ; Publication No. US20050260603A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MMI GENOMICS, INC.  
 ; APPLICANT: DENISE, Sue K.  
 ; APPLICANT: KERR, Richard  
 ; APPLICANT: ROSENFELD, David  
 ; APPLICANT: HOLM, Tom  
 ; APPLICANT: BATES, Stephen  
 ; APPLICANT: FANTIN, Dennis  
 ; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
 ; FILE REFERENCE: MM1100-2  
 ; CURRENT APPLICATION NUMBER: US/10/750,185  
 ; CURRENT FILING DATE: 2003-12-31  
 ; PRIOR APPLICATION NUMBER: US 60/437,482  
 ; PRIOR FILING DATE: 2002-12-31  
 ; NUMBER OF SEQ ID NOS: 64922  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 61723  
 ; LENGTH: 670  
 ; TYPE: DNA  
 ; ORGANISM: Bovine 19866880649350  
 US-10-750-185-61723

Query Match 73.3%; Score 15.4; DB 7; Length 670;  
 Best Local Similarity 84.2%; Pred. No. 1.4e+02;  
 Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 CTGTGAGGAACTWCTGTCT 21  
 DB 508 CTGTGAGGAACTWCTGTCT 526

RESULT 43  
 US-10-750-623-61723  
 ; Sequence 61723, Application US/10750623  
 ; Publication No. US20050287531A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MMI GENOMICS, INC.  
 ; APPLICANT: DENISE, Sue K.  
 ; APPLICANT: KERR, Richard  
 ; APPLICANT: ROSENFELD, David  
 ; APPLICANT: HOLM, Tom  
 ; APPLICANT: BATES, Stephen  
 ; APPLICANT: FANTIN, Dennis  
 ; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
 ; FILE REFERENCE: MM1100-1

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; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 61723
; TYPE: DNA
; ORGANISM: Bovine 19866880649350
US-10-750-623-61723

Query Match      73.3%; Score 15.4; DB 7; Length 670;
Best Local Similarity 84.2%; Pred. No. 1.4e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      3 CTGTGAGGAAGTCTGCTCT 21
Db      508 CTGTGAGGAAGTCTGCTCT 526

RESULT 44
US-10-750-185-51706
; Sequence 51706, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 51706
; LENGTH: 1374
; TYPE: DNA
; ORGANISM: Bovine 19866881516841
US-10-750-185-51706

Query Match      73.3%; Score 15.4; DB 7; Length 1374;
Best Local Similarity 84.2%; Pred. No. 1.6e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      3 CTGTGAGGAAGTCTGCTCT 21
Db      737 CTGTGAGGAAGTCTGCTCT 755

RESULT 45
US-10-750-623-51706
; Sequence 51706, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 51706
; LENGTH: 1374
; TYPE: DNA
; ORGANISM: Bovine 19866881516841
US-10-750-623-51706

Query Match      73.3%; Score 15.4; DB 7; Length 1374;
Best Local Similarity 84.2%; Pred. No. 1.6e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      3 CTGTGAGGAAGTCTGCTCT 21
Db      737 CTGTGAGGAAGTCTGCTCT 755

RESULT 46
US-10-750-185-38999
; Sequence 38999, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 38999
; LENGTH: 1467
; TYPE: DNA
; ORGANISM: Bovine 19866880809379
US-10-750-185-38999

Query Match      73.3%; Score 15.4; DB 7; Length 1467;
Best Local Similarity 84.2%; Pred. No. 1.6e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CCCTGTGAGGAAGTCTGCTGT 19
Db      682 CCCTGTGAGGAAGTCTGCTGT 700

RESULT 47
US-10-750-623-38999
; Sequence 38999, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 38999
; LENGTH: 1467
; TYPE: DNA
; ORGANISM: Bovine 19866880809379
US-10-750-623-38999

Query Match      73.3%; Score 15.4; DB 7; Length 1467;
Best Local Similarity 84.2%; Pred. No. 1.6e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CCCTGTGAGGAAGTCTGCTGT 19
Db      682 CCCTGTGAGGAAGTCTGCTGT 700
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; SEQ ID NO 38999  
; LENGTH: 1467  
; TYPE: DNA  
; ORGANISM: Bovine 19866880809379  
US-10-750-623-38999

Query Match 73.3%; Score 15.4; DB 7; Length 1467;  
Best Local Similarity 84.2%; Pred. No. 1.6e+02;  
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAACCTWCTGT 19  
||||| : ||||| : |||||  
Db 682 CCTGTGGGTAACTTCTGT 700

## RESULT 48

US-11-136-527-2274/c  
; Sequence 2274, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2274  
; LENGTH: 1493  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-11-136-527-2274

Query Match 73.3%; Score 15.4; DB 8; Length 1493;  
Best Local Similarity 84.2%; Pred. No. 1.6e+02;  
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCTGTGAGGAACCTWCTGTC 20  
||||| : ||||| : |||||  
Db 782 CCTGTGAGGAATACTGTC 764

## RESULT 49

US-11-136-527-3734/c  
; Sequence 3734, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3734  
; LENGTH: 3443  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-11-136-527-3734

Query Match 73.3%; Score 15.4; DB 8; Length 3443;  
Best Local Similarity 84.2%; Pred. No. 1.9e+02;  
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCTGTGAGGAACCTWCTGTC 20  
||||| : ||||| : |||||  
Db 1862 CCTGTGAGGAATACTGTC 1844

RESULT 50  
US-10-821-234-277  
; Sequence 277, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234  
; CURRENT FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: pc\_seq\_genes Version 1.0  
; SEQ ID NO 277  
; LENGTH: 5506  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-821-234-277  
Query Match 73.3%; Score 15.4; DB 7; Length 5506;  
Best Local Similarity 84.2%; Pred. No. 2e+02;  
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAACCTWCTGT 19  
||||| : ||||| : |||||  
Db 2895 CCTGTGAGGCACCTTCTGT 2913

Search completed: January 27, 2006, 07:33:55  
Job time : 397 secs

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OM nucleic - nucleic search, using sw model

Run on: January 27, 2006, 05:37:30 ; Search time 348.5 Seconds  
(without alignments)  
498.298 Million cell updates/sec

Title: US-10-070-415A-1

Perfect score: 21

Sequence: 1 cccgtgtgggaactwtgtct 21

Scoring table: IDENTITY\_NUC

Gapop 10\_0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications NA\_Main:\*

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2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*

3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*

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7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*

8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*

9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*

10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	20.6	98.1	21	9	US-10-070-415A-1
3	20.6	98.1	21	9	US-10-070-415A-1
4	20.6	98.1	21	9	US-10-070-415A-1
5	20.6	98.1	21	9	US-10-070-415A-1
6	20.6	98.1	21	9	US-10-070-415A-1
7	20.6	98.1	21	9	US-10-070-415A-1
8	20.6	98.1	21	9	US-10-070-415A-1
9	20.6	98.1	21	9	US-10-070-415A-1
10	20.6	98.1	21	9	US-10-070-415A-1
11	20.6	98.1	21	9	US-10-070-415A-1
12	20.6	98.1	21	9	US-10-070-415A-1
13	20.6	98.1	21	9	US-10-070-415A-1
14	20.6	98.1	21	9	US-10-070-415A-1
15	20.6	98.1	21	9	US-10-070-415A-1
16	20.6	98.1	21	9	US-10-070-415A-1
17	20.6	98.1	21	9	US-10-070-415A-1
18	20.6	98.1	21	9	US-10-070-415A-1
19	20.6	98.1	21	9	US-10-070-415A-1
20	20.6	98.1	21	9	US-10-070-415A-1
21	20.6	98.1	21	9	US-10-070-415A-1
22	20.6	98.1	21	9	US-10-070-415A-1
23	20.6	98.1	21	9	US-10-070-415A-1



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US-09-782-361-1
; Sequence 1, Application US/09782361
; Patent No. US20020064778A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yu-Wen
; TITLE OF INVENTION: PRIMER-SPECIFIC AND MISPAIR EXTENSION ASSAY FOR IDENTIFYING GEN
; FILE REFERENCE: 2883-4757US
; CURRENT APPLICATION NUMBER: US/09/782,361
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: sense universal primer for PCR (first round)
US-09-782-361-1

Query Match          98.1%; Score 20.6; DB 3; Length 25;
Best Local Similarity 95.2%; Pred. No. 0.81;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
   |||||
Db 4 CCTGTGAGGAAGTCTGTCT 24

RESULT 6
US-09-294-121A-1
; Sequence 1, Application US/09294121A
; Patent No. US20020069422A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/294,121A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/256,568
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002

US-09-294-121A-1
; Sequence 1, Application US/09899082A
; Patent No. US20020106638A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/899,082A
; FILING DATE: 06-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/378,900
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/256,568
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8000

US-09-294-121A-1
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: HCV (Kato et al., 1992)
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: HCV
; MAP POSITION: Position -299 of 5' end
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..27
; OTHER INFORMATION: /standard name=
; OTHER INFORMATION: "Universal HCV primer HcPr98"
US-09-294-121A-1

Query Match          98.1%; Score 20.6; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.82;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
   |||||
Db 1 CCTGTGAGGAAGTCTGTCT 21

RESULT 7
US-09-899-082A-1
; Sequence 1, Application US/09899082A
; Patent No. US20020106638A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/899,082A
; FILING DATE: 06-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/378,900
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/256,568
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8000
```





```

; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHEetical: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: HCV (Kato et al., 1992)
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: HCV
; MAP POSITION: Position -299 of 5' end
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..27
; OTHER INFORMATION: /standard_name=
; "Universal HCV primer HcPr98"
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-899-044-1
Query Match 98.1%; Score 20.6; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.82; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
DB 1 CCTGTGAGGAAGTCTGTCT 21

RESULT 10
US-10-407-897-78
; Sequence 78, Application US/10407897
; Publication No. US20040072148A1
; GENERAL INFORMATION:
; APPLICANT: Ji, Jiuping
; APPLICANT: Manak, Mark
; APPLICANT: Gonzalez, Irene
; TITLE OF INVENTION: Simultaneous Detection of HBV, HCV, and HIV in Plasma Samples
; TITLE OF INVENTION: Using a Multiplex Capture Assay
; FILE REFERENCE: 1589.0280002
; CURRENT APPLICATION NUMBER: US/10/407,897
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 10/130,533
; PRIOR FILING DATE: 2002-11-17
; PRIOR APPLICATION NUMBER: PCT/US00/31738
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/165,916
; PRIOR FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Primer
US-10-407-897-78
Query Match 98.1%; Score 20.6; DB 7; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.82; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
DB 1 CCTGTGAGGAAGTCTGTCT 21

; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHEtical: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: HCV (Kato et al., 1992)
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: HCV
; MAP POSITION: Position -299 of 5' end
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..27
; OTHER INFORMATION: /standard_name=
; "Universal HCV primer HcPr98"
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-822-711-1
Query Match 98.1%; Score 20.6; DB 8; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.82; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
DB 1 CCTGTGAGGAAGTCTGTCT 21

RESULT 11
US-10-822-711-1
; Sequence 1, Application US/10822711
; Publication No. US20040191768A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/822,711
; FILING DATE: 13-Apr-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/899,082A
; FILING DATE: 06-Jul-2001
; APPLICATION NUMBER: US/09/378,900
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/256,568
; FILING DATE: 18-Jul-1994
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 28-Nov-1993
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-Aug-1993
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-Nov-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHEtical: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: HCV (Kato et al., 1992)
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: HCV
; MAP POSITION: Position -299 of 5' end
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..27
; OTHER INFORMATION: /standard_name=
; "Universal HCV primer HcPr98"
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-822-711-1
Query Match 98.1%; Score 20.6; DB 8; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.82; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
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Db 1 CCCTGTGAGGAAGTCTGTCT 21

RESULT 12  
US-10-363-177A-5  
; Sequence 5, Application US/10363177A  
; Publication No. US20050084851A1  
; GENERAL INFORMATION:  
; APPLICANT: Pyrosequencing AB  
; APPLICANT: The Board of Trustees of the Leland Stanford Junior University  
; APPLICANT: Ronaghi, Mostafa  
; APPLICANT: Pourmand, Nader  
; APPLICANT: Ekstrom, Bjorn  
; TITLE OF INVENTION: Method of nucleic acid typing and sequencing  
; FILE REFERENCE: Docket 14629  
; CURRENT APPLICATION NUMBER: US/10/363,177A  
; CURRENT FILING DATE: 2003-03-06  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 27  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1..7)  
; OTHER INFORMATION: Synthetic oligonucleotide HCV-PCR-OUTF

US-10-363-177A-5  
Query Match 98.1%; Score 20.6; DB 9; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.82;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAAGTCTGTCT 21  
Db 1 CCCTGTGAGGAAGTCTGTCT 21

RESULT 13  
US-10-070-415A-30  
; Sequence 30, Application US/10070415A  
; Publication No. US20040043379A1  
; GENERAL INFORMATION:  
; APPLICANT: HASHIMOTO, Koji  
; APPLICANT: ASHIMOTO, Michie  
; APPLICANT: MASHIRO, Shunji  
; APPLICANT: OOTA, Yasuhiko  
; TITLE OF INVENTION: DETECTION OF NUCLEIC ACID ASSOCIATED WITH DISEASE  
; FILE REFERENCE: 220633US2SRDPT  
; CURRENT APPLICATION NUMBER: US/10/070,415A  
; CURRENT FILING DATE: 2003-07-23  
; PRIOR APPLICATION NUMBER: PCT/JP02/02030  
; PRIOR FILING DATE: 2002-03-05  
; PRIOR APPLICATION NUMBER: JP 2001-090053  
; PRIOR FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: JP 2001-284112  
; PRIOR FILING DATE: 2001-09-18  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 30  
; LENGTH: 36  
; TYPE: DNA  
; ORGANISM: Homo sapiens

US-10-070-415A-30  
Query Match 98.1%; Score 20.6; DB 7; Length 36;  
Best Local Similarity 100.0%; Pred. No. 0.84;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAAGTCTGTCT 21  
Db 16 CCCTGTGAGGAAGTCTGTCT 36

RESULT 14

US-09-728-265-22/c  
; Sequence 22, Application US/09729265  
; Publication No. US20020182598A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, David Y.  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION METHOD:  
; TITLE OF INVENTION: RAMIFICATION-EXTENSION AMPLIFICATION METHOD (RAM)  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Stroock & Stroock & Lavan  
; STREET: 180 Maiden Lane  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10038  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PCDOS/MSDOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/728,265  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pokotilow, Steven B  
; REGISTRATION NUMBER: 26,405  
; REFERENCE/DOCKET NUMBER: Old 29545APCT/USA-B // New 251305/0018  
; TELEPHONE: 212806-6663  
; TELEFAX: 2128066006  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 45 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 1..45

US-09-728-265-22  
Query Match 98.1%; Score 20.6; DB 3; Length 45;  
Best Local Similarity 95.2%; Pred. No. 0.85;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAAGTCTGTCT 21  
Db 31 CCCTGTGAGGAAGTCTGTCT 11

RESULT 15  
US-09-978-261A-22/c  
; Sequence 22, Application US/09978261A  
; Publication No. US20030175706A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, David Y.  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION METHODS  
; FILE REFERENCE: A29545-A-PCT-USA-A 070165.0601  
; CURRENT APPLICATION NUMBER: US/09/978,261A  
; CURRENT FILING DATE: 2002-09-05  
; PRIOR APPLICATION NUMBER: 08/263,937  
; PRIOR FILING DATE: 1994-06-22  
; PRIOR APPLICATION NUMBER: 08/596,331  
; PRIOR FILING DATE: 1996-02-22  
; PRIOR APPLICATION NUMBER: 08/690,495  
; PRIOR FILING DATE: 1996-07-31  
; PRIOR APPLICATION NUMBER: 08/909,031  
; PRIOR FILING DATE: 1997-08-11

; PRIOR APPLICATION NUMBER: 09/728,265  
; PRIOR FILING DATE: 2000-12-01  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 22  
; LENGTH: 45  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide probe  
US-09-978-261A-22

Query Match 98.1%; Score 20.6; DB 3; Length 45;  
Best Local Similarity 95.2%; Pred. No. 0.85;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21  
|||  
Db 31 CCTGTGAGGAAGTCTGTCT 11

RESULT 16  
US-10-309-438-22/c  
; Sequence 22, Application US/10309438  
; Publication No. US20030190604A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, David Y.  
; APPLICANT: Brandwein, Maragat  
; APPLICANT: Heuh, Terence C.H.  
; TITLE OF INVENTION: Nucleic Acid Amplification Method: Ramification-extension  
; FILE REFERENCE: 251305/0031  
; CURRENT APPLICATION NUMBER: US/10/309,438  
; PRIOR FILING DATE: 2003-04-08  
; PRIOR FILING DATE: 1999-04-23  
; PRIOR APPLICATION NUMBER: US 09/299,217  
; PRIOR FILING DATE: 1996-07-31  
; PRIOR APPLICATION NUMBER: US 08/690,494  
; PRIOR FILING DATE: 1996-05-20  
; PRIOR APPLICATION NUMBER: PCT/US95/07671  
; PRIOR FILING DATE: 1995-06-14  
; PRIOR APPLICATION NUMBER: 08/263,937  
; PRIOR FILING DATE: 1994-06-22  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 22  
; LENGTH: 45  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide probe  
US-10-309-438-22

Query Match 98.1%; Score 20.6; DB 6; Length 45;  
Best Local Similarity 95.2%; Pred. No. 0.85;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21  
|||  
Db 31 CCTGTGAGGAAGTCTGTCT 11

RESULT 17  
US-10-719-480-22/c  
; Sequence 22, Application US/10719480  
; Publication No. US20040137484A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, David Y.  
; APPLICANT: Yi, Jizu  
; APPLICANT: Zhang, Wandu  
; TITLE OF INVENTION: Nucleic Acid Amplification Methods  
; FILE REFERENCE: 251305/0040

; CURRENT APPLICATION NUMBER: US/10/719,480  
; CURRENT FILING DATE: 2003-11-21  
; PRIOR APPLICATION NUMBER: US 09/978,261  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: PCT/US02/32754  
; PRIOR FILING DATE: 2002-10-11  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 22  
; LENGTH: 45  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide probe  
US-10-719-480-22

Query Match 98.1%; Score 20.6; DB 7; Length 45;  
Best Local Similarity 95.2%; Pred. No. 0.85;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21  
|||  
Db 31 CCTGTGAGGAAGTCTGTCT 11

RESULT 18  
US-10-451-882-41  
; Sequence 41, Application US/10451882  
; Publication No. US20040185455A1  
; GENERAL INFORMATION:  
; APPLICANT: Takara Shuzo Co., Ltd.  
; TITLE OF INVENTION: Method for detection of virulent organisms  
; FILE REFERENCE: 662981  
; CURRENT APPLICATION NUMBER: US/10/451,882  
; CURRENT FILING DATE: 2004-01-05  
; PRIOR APPLICATION NUMBER: JP 2000-396321  
; PRIOR FILING DATE: 2000-12-26  
; PRIOR APPLICATION NUMBER: JP 2000-396222  
; PRIOR FILING DATE: 2000-12-26  
; PRIOR APPLICATION NUMBER: JP 2001-199552  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: JP 2001-278920  
; PRIOR FILING DATE: 2001-09-13  
; NUMBER OF SEQ ID NOS: 44  
; SEQ ID NO 41  
; LENGTH: 73  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer area to amplify a portion of HCV.  
US-10-451-882-41

Query Match 98.1%; Score 20.6; DB 8; Length 73;  
Best Local Similarity 95.2%; Pred. No. 0.88;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21  
|||  
Db 21 CCTGTGAGGAAGTCTGTCT 41

RESULT 19  
US-10-333-449A-28  
; Sequence 28, Application US/10333449A  
; Publication No. US20040137424A1  
; GENERAL INFORMATION:  
; APPLICANT: Tan, Yin Hwee  
; APPLICANT: Lim, Siew Pheng  
; APPLICANT: Lim, Seng Gee  
; APPLICANT: Hong, Wan Jin  
; TITLE OF INVENTION: NUCLEIC ACIDS AND METHODS FOR DETECTING VIRAL INFECTION,  
; TITLE OF INVENTION: UNCOVERING ANTI-VIRAL DRUG CANDIDATES AND DETERMINING DRUG  
; FILE REFERENCE: RESISTANCE OF VIRAL ISOLATES

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; FILE REFERENCE: 01/22137
; CURRENT APPLICATION NUMBER: US/10/333,449A
; CURRENT FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 85
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Single strand DNA oligonucleotide
US-10-333-449A-28

Query Match          98.1%; Score 20.6; DB 7; Length 85;
Best Local Similarity 95.2%; Pred. No. 0.89;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
Db 43 CCCTGTGAGGAAGTCTGTCT 63

RESULT 20
US-10-318-416B-15
; Sequence 15, Application US/10318416B
; Publication No. US20040115643A1
; GENERAL INFORMATION:
; APPLICANT: Lizardi, Paul M.
; APPLICANT: Gribanov, Oleg G.
; TITLE OF INVENTION: THERMODYNAMIC EQUILIBRIUM EXTENSION OF
; TITLE OF INVENTION: PRIMERS
; FILE REFERENCE: 25006.001201
; CURRENT APPLICATION NUMBER: US/10/318,416B
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 110
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence./note =
; OTHER INFORMATION: synthetic construct
US-10-318-416B-15

Query Match          98.1%; Score 20.6; DB 7; Length 110;
Best Local Similarity 95.2%; Pred. No. 0.91;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
Db 11 CCCTGTGAGGAAGTCTGTCT 31

RESULT 21
US-09-345-761-4
; Sequence 4, Application US/09345761
; Patent No. US20010053518A1
; GENERAL INFORMATION:
; APPLICANT: ISHIGURO, Takahiko
; APPLICANT: SAITOH, Juichi
; APPLICANT: ISHIZUKA, Tetsuya
; TITLE OF INVENTION: METHOD OF ASSAY OF TARGET NUCLEIC ACID
; FILE REFERENCE: Q54969
; CURRENT APPLICATION NUMBER: US/09/345,761
; CURRENT FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: JP 10-186434
; PRIOR FILING DATE: 1998-07-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 133
; TYPE: RNA
; ORGANISM: Hepatitis C virus
; FEATURE:
; OTHER INFORMATION:
US-09-345-761-4

Query Match          98.1%; Score 20.6; DB 9; Length 267;
Best Local Similarity 95.2%; Pred. No. 0.98;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
Db 93 CCCTGTGAGGAAGTCTGTCT 113

RESULT 22
US-10-687-588-4
; Sequence 4, Application US/10687588
; Publication No. US20040115718A1
; GENERAL INFORMATION:
; APPLICANT: ISHIGURO, Takahiko
; APPLICANT: SAITOH, Juichi
; APPLICANT: ISHIZUKA, Tetsuya
; TITLE OF INVENTION: METHOD OF ASSAY OF TARGET NUCLEIC ACID
; FILE REFERENCE: Q54969
; CURRENT APPLICATION NUMBER: US/10/687,588
; CURRENT FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: US/09/345,761
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: JP 10-186434
; PRIOR FILING DATE: 1998-07-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 133
; TYPE: RNA
; ORGANISM: synthetic construct
US-10-687-588-4

Query Match          98.1%; Score 20.6; DB 7; Length 133;
Best Local Similarity 66.7%; Pred. No. 0.93;
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
Db 93 CCCTGTGAGGAAGTCTGTCT 113

RESULT 23
US-10-363-177A-69
; Sequence 69, Application US/10363177A
; Publication No. US20050084851A1
; GENERAL INFORMATION:
; APPLICANT: Pyrosequencing AB
; APPLICANT: The Board of Trustees of the Leland Stanford Junior University
; APPLICANT: Ronaghi, Mostafa
; APPLICANT: Pourmand, Nader
; APPLICANT: Ekstrom, Bjorn
; TITLE OF INVENTION: Method of nucleic acid typing and sequencing
; FILE REFERENCE: Docket 14629
; CURRENT APPLICATION NUMBER: US/10/363,177A
; CURRENT FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 69
; LENGTH: 267
; TYPE: DNA
; ORGANISM: Hepatitis C virus
; FEATURE:
; OTHER INFORMATION:
US-10-363-177A-69

Query Match          98.1%; Score 20.6; DB 9; Length 267;
Best Local Similarity 95.2%; Pred. No. 0.98;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
Db 93 CCCTGTGAGGAAGTCTGTCT 113

```

```
Db      1 CCCTGTGAGGAACCTCTGTCT 21

RESULT 24
US-10-363-177A-67
; Sequence 67, Application US/10363177A
; Publication No. US20050084851A1
; GENERAL INFORMATION:
; APPLICANT: Pyrosequencing AB
; APPLICANT: The Board of Trustees of the Leland Stanford Junior University
; APPLICANT: Ronaghi, Mostafa
; APPLICANT: Pourmand, Nader
; APPLICANT: Ekstrom, Bjorn
; TITLE OF INVENTION: Method of nucleic acid typing and sequencing
; FILE REFERENCE: Docket 14629
; CURRENT APPLICATION NUMBER: US/10/363,177A
; CURRENT FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
; LENGTH: 278
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-10-363-177A-67

Query Match      98.1%; Score 20.6; DB 9; Length 278;
Best Local Similarity 95.2%; Pred. No. 0.98;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCCTGTGAGGAACCTCTGTCT 21
        |||||:|||||:|||||:|||||:
Db      1 CCCTGTGAGGAACCTCTGTCT 21

RESULT 25
US-09-345-761-7
; Sequence 7, Application US/09345761
; Patent No. US20010053518A1
; GENERAL INFORMATION:
; APPLICANT: SAITOH, Juichi
; APPLICANT: ISHIGURO, Takahiko
; APPLICANT: ISHIZUKA, Tetsuya
; TITLE OF INVENTION: METHOD OF ASSAY OF TARGET NUCLEIC ACID
; FILE REFERENCE: Q54969
; CURRENT APPLICATION NUMBER: US/09/345,761
; CURRENT FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: JP 10-186434
; PRIOR FILING DATE: 1998-07-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 298
; TYPE: RNA
; ORGANISM: Synthetic Construct
US-09-345-761-7

Query Match      98.1%; Score 20.6; DB 3; Length 298;
Best Local Similarity 66.7%; Pred. No. 0.99;
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCCTGTGAGGAACCTCTGTCT 21
        |||||:|||||:|||||:|||||:
Db      29 CCCUGUGAGGAACUACUGUCU 49

RESULT 26
US-10-687-588-7
; Sequence 7, Application US/10687588
; Publication No. US20040115718A1
; GENERAL INFORMATION:
; APPLICANT: ISHIGURO, Takahiko
; APPLICANT: SAITOH, Juichi
; APPLICANT: ISHIZUKA, Tetsuya
```

```
; TITLE OF INVENTION: METHOD OF ASSAY OF TARGET NUCLEIC ACID
; FILE REFERENCE: Q54969
; CURRENT APPLICATION NUMBER: US/10/687,588
; CURRENT FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: US/09/345,761
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: JP 10-186434
; PRIOR FILING DATE: 1998-07-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 298
; TYPE: RNA
; ORGANISM: Synthetic Construct
US-10-687-588-7

Query Match      98.1%; Score 20.6; DB 7; Length 298;
Best Local Similarity 66.7%; Pred. No. 0.99;
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCCTGTGAGGAACCTCTGTCT 21
        |||||:|||||:|||||:|||||:
Db      29 CCCUGUGAGGAACUACUGUCU 49

RESULT 27
US-10-230-381-1
; Sequence 1, Application US/10230381
; Publication No. US20030152591A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: New hepatitis C virus genotype 13, and its use as prophylactic,
; FILE REFERENCE: INN-124-EP
; CURRENT APPLICATION NUMBER: US/10/230,381
; CURRENT FILING DATE: 2002-08-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 299
; TYPE: DNA
; ORGANISM: hepatitis C virus
US-10-230-381-1

Query Match      98.1%; Score 20.6; DB 6; Length 299;
Best Local Similarity 95.2%; Pred. No. 0.99;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCCTGTGAGGAACCTCTGTCT 21
        |||||:|||||:|||||:|||||:
Db      1 CCCTGTGAGGAACCTCTGTCT 21

RESULT 28
US-10-363-177A-63
; Sequence 63, Application US/10363177A
; Publication No. US20050084851A1
; GENERAL INFORMATION:
; APPLICANT: Pyrosequencing AB
; APPLICANT: The Board of Trustees of the Leland Stanford Junior University
; APPLICANT: Ronaghi, Mostafa
; APPLICANT: Pourmand, Nader
; APPLICANT: Ekstrom, Bjorn
; TITLE OF INVENTION: Method of nucleic acid typing and sequencing
; FILE REFERENCE: Docket 14629
; CURRENT APPLICATION NUMBER: US/10/363,177A
; CURRENT FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 63
; LENGTH: 305
; TYPE: DNA
; ORGANISM: Hepatitis C virus
```

US-10-363-177A-63

Query Match 98.1%; Score 20.6; DB 9; Length 305;  
 Best Local Similarity 95.2%; Pred. No. 0.99;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21  
 |||||  
 DB 1 CCTGTGAGGAAGTCTGTCT 21

RESULT 29

US-10-363-177A-64  
 ; Sequence 64, Application US/10363177A  
 ; Publication No. US20050084851A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pyrosequencing AB  
 ; APPLICANT: The Board of Trustees of the Leland Stanford Junior University  
 ; APPLICANT: Ronaghi, Mostafa  
 ; APPLICANT: Pourmand, Nader  
 ; APPLICANT: Ekstrom, Bjorn  
 ; TITLE OF INVENTION: Method of nucleic acid typing and sequencing  
 ; FILE REFERENCE: Docket 14629  
 ; CURRENT APPLICATION NUMBER: US/10/363,177A  
 ; CURRENT FILING DATE: 2003-03-06  
 ; NUMBER OF SEQ ID NOS: 72  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 64  
 ; LENGTH: 305  
 ; TYPE: DNA  
 ; ORGANISM: Hepatitis C virus  
 US-10-363-177A-64

Query Match 98.1%; Score 20.6; DB 9; Length 305;  
 Best Local Similarity 95.2%; Pred. No. 0.99;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21  
 |||||  
 DB 1 CCTGTGAGGAAGTCTGTCT 21

RESULT 30

US-10-363-177A-65  
 ; Sequence 65, Application US/10363177A  
 ; Publication No. US20050084851A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pyrosequencing AB  
 ; APPLICANT: The Board of Trustees of the Leland Stanford Junior University  
 ; APPLICANT: Ronaghi, Mostafa  
 ; APPLICANT: Pourmand, Nader  
 ; APPLICANT: Ekstrom, Bjorn  
 ; TITLE OF INVENTION: Method of nucleic acid typing and sequencing  
 ; FILE REFERENCE: Docket 14629  
 ; CURRENT APPLICATION NUMBER: US/10/363,177A  
 ; CURRENT FILING DATE: 2003-03-06  
 ; NUMBER OF SEQ ID NOS: 72  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 65  
 ; LENGTH: 305  
 ; TYPE: DNA  
 ; ORGANISM: Hepatitis C virus  
 US-10-363-177A-65

Query Match 98.1%; Score 20.6; DB 9; Length 305;  
 Best Local Similarity 95.2%; Pred. No. 0.99;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21  
 |||||  
 DB 1 CCTGTGAGGAAGTCTGTCT 21

RESULT 31

US-10-363-177A-66  
 ; Sequence 66, Application US/10363177A  
 ; Publication No. US20050084851A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pyrosequencing AB  
 ; APPLICANT: The Board of Trustees of the Leland Stanford Junior University  
 ; APPLICANT: Ronaghi, Mostafa  
 ; APPLICANT: Pourmand, Nader  
 ; APPLICANT: Ekstrom, Bjorn  
 ; TITLE OF INVENTION: Method of nucleic acid typing and sequencing  
 ; FILE REFERENCE: Docket 14629  
 ; CURRENT APPLICATION NUMBER: US/10/363,177A  
 ; CURRENT FILING DATE: 2003-03-06  
 ; NUMBER OF SEQ ID NOS: 72  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 66  
 ; LENGTH: 305  
 ; TYPE: DNA  
 ; ORGANISM: Hepatitis C virus  
 US-10-363-177A-66

Query Match 98.1%; Score 20.6; DB 9; Length 305;  
 Best Local Similarity 95.2%; Pred. No. 0.99;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21  
 |||||  
 DB 1 CCTGTGAGGAAGTCTGTCT 21

RESULT 32

US-10-363-177A-68  
 ; Sequence 68, Application US/10363177A  
 ; Publication No. US20050084851A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pyrosequencing AB  
 ; APPLICANT: The Board of Trustees of the Leland Stanford Junior University  
 ; APPLICANT: Ronaghi, Mostafa  
 ; APPLICANT: Pourmand, Nader  
 ; APPLICANT: Ekstrom, Bjorn  
 ; TITLE OF INVENTION: Method of nucleic acid typing and sequencing  
 ; FILE REFERENCE: Docket 14629  
 ; CURRENT APPLICATION NUMBER: US/10/363,177A  
 ; CURRENT FILING DATE: 2003-03-06  
 ; NUMBER OF SEQ ID NOS: 72  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 68  
 ; LENGTH: 305  
 ; TYPE: DNA  
 ; ORGANISM: Hepatitis C virus  
 US-10-363-177A-68

Query Match 98.1%; Score 20.6; DB 9; Length 305;  
 Best Local Similarity 95.2%; Pred. No. 0.99;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21  
 |||||  
 DB 1 CCTGTGAGGAAGTCTGTCT 21

RESULT 33

US-09-345-761-6  
 ; Sequence 6, Application US/09345761  
 ; Patent No. US20010053518A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ISHIGURO, Takahiko  
 ; APPLICANT: SAITOH, Juichi  
 ; APPLICANT: ISHIZUKA, Tetsuya  
 ; TITLE OF INVENTION: METHOD OF ASSAY OF TARGET NUCLEIC ACID  
 ; FILE REFERENCE: Q54969  
 ; CURRENT APPLICATION NUMBER: US/09/345,761

; CURRENT FILING DATE: 1999-07-01  
 ; PRIOR APPLICATION NUMBER: JP 10-186434  
 ; PRIOR FILING DATE: 1998-07-01  
 ; NUMBER OF SEQ ID NOS: 7  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 6  
 ; LENGTH: 315  
 ; TYPE: DNA  
 ; ORGANISM: Synthetic Construct  
 US-09-345-761-6

Query Match 98.1%; Score 20.6; DB 3; Length 315;  
 Best Local Similarity 95.2%; Pred. No. 0.99;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21  
 |||||:|||||:|||||:  
 DB 46 CCCTGTGAGGAAGTCTGTCT 66

RESULT 34  
 US-10-687-588-6  
 ; Sequence 6, Application US/10687588  
 ; Publication No. US20040115718A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ISHIGURO, Takahiko  
 ; APPLICANT: SAITOH, Juichi  
 ; APPLICANT: ISHIZUKA, Tetsuya  
 ; TITLE OF INVENTION: METHOD OF ASSAY OF TARGET NUCLEIC ACID  
 ; FILE REFERENCE: Q54969  
 ; CURRENT APPLICATION NUMBER: US/10/687,588  
 ; CURRENT FILING DATE: 2003-10-20  
 ; PRIOR APPLICATION NUMBER: US/09/345,761  
 ; PRIOR FILING DATE: 1999-07-01  
 ; PRIOR APPLICATION NUMBER: JP 10-186434  
 ; PRIOR FILING DATE: 1998-07-01  
 ; NUMBER OF SEQ ID NOS: 7  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 6  
 ; LENGTH: 315  
 ; TYPE: DNA  
 ; ORGANISM: Synthetic Construct  
 US-10-687-588-6

Query Match 98.1%; Score 20.6; DB 7; Length 315;  
 Best Local Similarity 95.2%; Pred. No. 0.99;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21  
 |||||:|||||:|||||:  
 DB 46 CCCTGTGAGGAAGTCTGTCT 66

RESULT 35  
 US-09-882-945A-240  
 ; Sequence 240, Application US/09882945A  
 ; Publication No. US20030143535A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lyamichev, Victor  
 ; APPLICANT: Allawi, Hatim  
 ; APPLICANT: Dong, Fang  
 ; APPLICANT: Neri, Bruce  
 ; APPLICANT: Vener, Tatiana  
 ; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites  
 ; FILE REFERENCE: FORS-04586  
 ; CURRENT APPLICATION NUMBER: US/09/882,945A  
 ; CURRENT FILING DATE: 2001-06-15  
 ; NUMBER OF SEQ ID NOS: 334  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 240  
 ; LENGTH: 328  
 ; TYPE: RNA  
 ; ORGANISM: Hepatitis C virus

US-09-882-945A-240

Query Match 98.1%; Score 20.6; DB 3; Length 328;  
 Best Local Similarity 66.7%; Pred. No. 0.99;  
 Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21  
 |||||:|||||:|||||:  
 DB 25 CCUGUGAGGAACUACUGUCU 45

RESULT 36  
 US-09-882-945A-242  
 ; Sequence 242, Application US/09882945A  
 ; Publication No. US20030143535A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lyamichev, Victor  
 ; APPLICANT: Allawi, Hatim  
 ; APPLICANT: Dong, Fang  
 ; APPLICANT: Neri, Bruce  
 ; APPLICANT: Vener, Tatiana  
 ; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites  
 ; FILE REFERENCE: FORS-04586  
 ; CURRENT APPLICATION NUMBER: US/09/882,945A  
 ; CURRENT FILING DATE: 2001-06-15  
 ; NUMBER OF SEQ ID NOS: 334  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 242  
 ; LENGTH: 328  
 ; TYPE: RNA  
 ; ORGANISM: Hepatitis C virus  
 US-09-882-945A-242

Query Match 98.1%; Score 20.6; DB 3; Length 328;  
 Best Local Similarity 66.7%; Pred. No. 0.99;  
 Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21  
 |||||:|||||:|||||:  
 DB 25 CCUGUGAGGAACUACUGUCU 45

RESULT 37  
 US-09-882-945A-243  
 ; Sequence 243, Application US/09882945A  
 ; Publication No. US20030143535A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lyamichev, Victor  
 ; APPLICANT: Allawi, Hatim  
 ; APPLICANT: Dong, Fang  
 ; APPLICANT: Neri, Bruce  
 ; APPLICANT: Vener, Tatiana  
 ; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites  
 ; FILE REFERENCE: FORS-04586  
 ; CURRENT APPLICATION NUMBER: US/09/882,945A  
 ; CURRENT FILING DATE: 2001-06-15  
 ; NUMBER OF SEQ ID NOS: 334  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 243  
 ; LENGTH: 328  
 ; TYPE: RNA  
 ; ORGANISM: Hepatitis C virus  
 US-09-882-945A-243

Query Match 98.1%; Score 20.6; DB 3; Length 328;  
 Best Local Similarity 66.7%; Pred. No. 0.99;  
 Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21  
 |||||:|||||:|||||:  
 DB 25 CCUGUGAGGAACUACUGUCU 45

```

RESULT 38
US-09-882-945A-245
; Sequence 245, Application US/09882945A
; Publication No. US20030143535A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Allawi, Hatim
; APPLICANT: Dong, Fang
; APPLICANT: Neri, Bruce
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/09/882,945A
; CURRENT FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 245
; LENGTH: 328
; TYPE: RNA
; ORGANISM: Hepatitis C virus
US-09-882-945A-245

Query Match          98.1%; Score 20.6; DB 3; Length 328;
Best Local Similarity 66.7%; Pred. No. 0.99;
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCCTGTGAGGAAGTCTGTCT 21
Db      25 CCCUGAGGAGAACUACUGUCU 45

RESULT 39
US-10-475-024-18
; Sequence 18, Application US/10475024
; Publication No. US20040219545A1
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; APPLICANT: Welch, Ellen
; TITLE OF INVENTION: METHODS FOR IDENTIFYING SMALL MOLECULES THAT BIND SPECIFIC RNA
; FILE REFERENCE: 10589-007-999
; CURRENT APPLICATION NUMBER: US/10/475,024
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 60/282,965
; PRIOR FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 328
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-475-024-18

Query Match          98.1%; Score 20.6; DB 8; Length 328;
Best Local Similarity 66.7%; Pred. No. 0.99;
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCCTGTGAGGAAGTCTGTCT 21
Db      31 CCCUGAGGAGAACUACUGUCU 51

RESULT 40
US-10-807-114-240
; Sequence 240, Application US/10807114
; Publication No. US20040235024A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Allawi, Hatim
; APPLICANT: Dong, Fang
; APPLICANT: Neri, Bruce
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites

```

```

; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/10/807,114
; CURRENT FILING DATE: 2004-03-23
; PRIOR APPLICATION NUMBER: US/09/882,945
; PRIOR FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 240
; LENGTH: 328
; TYPE: RNA
; ORGANISM: Hepatitis C virus
US-10-807-114-240

Query Match          98.1%; Score 20.6; DB 8; Length 328;
Best Local Similarity 66.7%; Pred. No. 0.99;
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCCTGTGAGGAAGTCTGTCT 21
Db      25 CCCUGAGGAGAACUACUGUCU 45

RESULT 41
US-10-807-114-242
; Sequence 242, Application US/10807114
; Publication No. US20040235024A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Allawi, Hatim
; APPLICANT: Dong, Fang
; APPLICANT: Neri, Bruce
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/10/807,114
; CURRENT FILING DATE: 2004-03-23
; PRIOR APPLICATION NUMBER: US/09/882,945
; PRIOR FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 242
; LENGTH: 328
; TYPE: RNA
; ORGANISM: Hepatitis C virus
US-10-807-114-242

Query Match          98.1%; Score 20.6; DB 8; Length 328;
Best Local Similarity 66.7%; Pred. No. 0.99;
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCCTGTGAGGAAGTCTGTCT 21
Db      25 CCCUGAGGAGAACUACUGUCU 45

RESULT 42
US-10-807-114-243
; Sequence 243, Application US/10807114
; Publication No. US20040235024A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Allawi, Hatim
; APPLICANT: Dong, Fang
; APPLICANT: Neri, Bruce
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/10/807,114
; CURRENT FILING DATE: 2004-03-23
; PRIOR APPLICATION NUMBER: US/09/882,945
; PRIOR FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn version 3.0

```



; SEQ ID NO 243  
; LENGTH: 328  
; TYPE: RNA  
; ORGANISM: Hepatitis C virus  
US-10-807-114-243

Query Match 98.1%; Score 20.6; DB 8; Length 328;  
Best Local Similarity 66.7%; Pred. No. 0.99;  
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAACACTWCTGTCT 21  
|||:|||||:|:|:|:|:|:|:  
Db 25 CCUGUGAGGAACUACUGUCU 45

## RESULT 43

US-10-807-114-245  
; Sequence 245, Application US/10807114  
; Publication No. US20040235024A1  
; GENERAL INFORMATION:  
; APPLICANT: Iyamichev, Victor  
; APPLICANT: Allawi, Hatim  
; APPLICANT: Dong, Fang  
; APPLICANT: Neri, Bruce  
; APPLICANT: Vener, Tatiana  
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites  
; FILE REFERENCE: FORS-04586  
; CURRENT APPLICATION NUMBER: US/10/807,114  
; CURRENT FILING DATE: 2004-03-23  
; PRIOR APPLICATION NUMBER: US/09/882,945  
; PRIOR FILING DATE: 2001-06-15  
; NUMBER OF SEQ ID NOS: 334  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 245  
; LENGTH: 328  
; TYPE: RNA  
; ORGANISM: Hepatitis C virus  
US-10-807-114-245

Query Match 98.1%; Score 20.6; DB 8; Length 328;  
Best Local Similarity 66.7%; Pred. No. 0.99;  
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAACACTWCTGTCT 21  
|||:|||||:|:|:|:|:|:|:  
Db 25 CCUGUGAGGAACUACUGUCU 45

## RESULT 44

US-10-475-026-18  
; Sequence 18, Application US/10475026  
; Publication No. US20050142545A1  
; GENERAL INFORMATION:  
; APPLICANT: Conn, Michael Morgan  
; APPLICANT: Pelligrini, Mathew  
; APPLICANT: Hwang, Seongwoo  
; APPLICANT: Moon, Young-choon  
; APPLICANT: Almstead, Neil  
; TITLE OF INVENTION: METHODS FOR IDENTIFYING SMALL MOLECULES THAT BIND SPECIFIC RNA  
; FILE REFERENCE: 10589-008  
; CURRENT APPLICATION NUMBER: US/10/475,026  
; CURRENT FILING DATE: 2003-10-10  
; PRIOR APPLICATION NUMBER: 60/282,966  
; PRIOR FILING DATE: 2001-04-11  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 18  
; LENGTH: 328  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-475-026-18

Query Match 98.1%; Score 20.6; DB 9; Length 328;  
Best Local Similarity 66.7%; Pred. No. 0.99;  
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAACACTWCTGTCT 21  
|||:|||||:|:|:|:|:|:|:  
Db 31 CCUGUGAGGAACUACUGUCU 51

## RESULT 45

US-09-814-292-44  
; Sequence 44, Application US/09814292  
; Patent No. US20020120117A1  
; GENERAL INFORMATION:  
; APPLICANT: Yu, De-Chao  
; APPLICANT: Zhang, Hong  
; APPLICANT: Henderson, Daniel R.  
; TITLE OF INVENTION: HUMAN UROTHELIAL CELL SPECIFIC UROPLAKIN  
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATORY SEQUENCES, VECTORS COMPRISING  
; TITLE OF INVENTION: UROPLAKIN-SPECIFIC TRANSCRIPTIONAL REGULATORY SEQUENCES, AND  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 348022001500  
; CURRENT APPLICATION NUMBER: US/09/814,292  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: 60/191,861  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 44  
; LENGTH: 341  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: 5' UTR region of HCV  
US-09-814-292-44

Query Match 98.1%; Score 20.6; DB 3; Length 341;  
Best Local Similarity 95.2%; Pred. No. 1;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAACACTWCTGTCT 21  
|||:|||||:|:|:~|:|:|:|:|:|:  
Db 43 CCCTGTGAGGAACACTGTCT 63

## RESULT 46

US-09-814-357-3  
; Sequence 3, Application US/09814357  
; Publication No. US20030068307A1  
; GENERAL INFORMATION:  
; APPLICANT: Yu, De-Chao  
; APPLICANT: Chen, Yu  
; APPLICANT: Henderson, Daniel R.  
; TITLE OF INVENTION: METHODS OF TREATING NEOPLASIA  
; TITLE OF INVENTION: WITH COMBINATION TARGET CELL-SPECIFIC ADENOVIRUS,  
; TITLE OF INVENTION: CHEMOTHERAPY AND RADIATION  
; FILE REFERENCE: 348022001600  
; CURRENT APPLICATION NUMBER: US/09/814,357  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 60/192,015  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 341  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: 5' UTR region of HCV  
US-09-814-357-3

Query Match 98.1%; Score 20.6; DB 3; Length 341;  
Best Local Similarity 95.2%; Pred. No. 1;

Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21  
 |||||  
 Db 43 CCTGTGAGGAAGTCTGTCT 63

RESULT 47  
 US-09-814-351-3  
 ; Sequence 3, Application US/09814351  
 ; Publication No. US20030148520A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yu, De-Chao  
 ; APPLICANT: Li, Yuanhao  
 ; APPLICANT: Henderson, Daniel R.  
 ; TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTORS  
 ; FILE OF INVENTION: COMPRISING AN INTERNAL RIBOSOME ENTRY SITE  
 ; FILE REFERENCE: 348022001700  
 ; CURRENT APPLICATION NUMBER: US/09/814,351  
 ; CURRENT FILING DATE: 2001-03-21  
 ; PRIOR APPLICATION NUMBER: 60/192,156  
 ; PRIOR FILING DATE: 2000-03-24  
 ; NUMBER OF SEQ ID NOS: 35  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 3  
 ; LENGTH: 341  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: 5' UTR region of HCV  
 US-09-814-351-3

Query Match 98.1%; Score 20.6; DB 3; Length 341;  
 Best Local Similarity 95.2%; Pred. No. 1;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21  
 |||||  
 Db 43 CCTGTGAGGAAGTCTGTCT 63

RESULT 48  
 US-10-259-275-35  
 ; Sequence 35, Application US/10259275  
 ; Publication No. US20030125541A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lemon, Stanley M.  
 ; APPLICANT: Yi, Minkyung  
 ; TITLE OF INVENTION: REPLICATION COMPETENT HEPATITIS C VIRUS AND METHODS OF USE  
 ; FILE REFERENCE: 265.0007 0120  
 ; CURRENT APPLICATION NUMBER: US/10/259,275  
 ; CURRENT FILING DATE: 2003-01-13  
 ; PRIOR APPLICATION NUMBER: US 60/171,909  
 ; PRIOR FILING DATE: 1999-12-23  
 ; PRIOR APPLICATION NUMBER: US 09/747,419  
 ; PRIOR FILING DATE: 2000-12-23  
 ; PRIOR APPLICATION NUMBER: US 60/325,236  
 ; PRIOR FILING DATE: 2001-09-27  
 ; PRIOR APPLICATION NUMBER: US 60/338,123  
 ; PRIOR FILING DATE: 2001-11-13  
 ; NUMBER OF SEQ ID NOS: 73  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 35  
 ; LENGTH: 341  
 ; TYPE: DNA  
 ; ORGANISM: ARTIFICIAL  
 ; FEATURE:  
 ; OTHER INFORMATION: nucleotide sequence of 5' NTR  
 US-10-259-275-35

Query Match 98.1%; Score 20.6; DB 6; Length 341;  
 Best Local Similarity 95.2%; Pred. No. 1;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21  
 |||||  
 Db 43 CCTGTGAGGAAGTCTGTCT 63

RESULT 49  
 US-10-691-045-3  
 ; Sequence 3, Application US/10691045  
 ; Publication No. US20040146489A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yu, De-Chao  
 ; APPLICANT: Li, Yuanhao  
 ; APPLICANT: Henderson, Daniel R.  
 ; TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTORS  
 ; FILE OF INVENTION: COMPRISING AN INTERNAL RIBOSOME ENTRY SITE  
 ; FILE REFERENCE: 348022001700  
 ; CURRENT APPLICATION NUMBER: US/10/691,045  
 ; CURRENT FILING DATE: 2003-10-21  
 ; PRIOR APPLICATION NUMBER: US/09/814,351  
 ; PRIOR FILING DATE: 2001-03-21  
 ; PRIOR APPLICATION NUMBER: 60/192,156  
 ; PRIOR FILING DATE: 2000-03-24  
 ; NUMBER OF SEQ ID NOS: 35  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 3  
 ; LENGTH: 341  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: 5' UTR region of HCV  
 US-10-691-045-3

Query Match 98.1%; Score 20.6; DB 7; Length 341;  
 Best Local Similarity 95.2%; Pred. No. 1;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21  
 |||||  
 Db 43 CCTGTGAGGAAGTCTGTCT 63

RESULT 50  
 US-11-006-313-35  
 ; Sequence 35, Application US/11006313  
 ; Publication No. US20050153281A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lemon, Stanley M.  
 ; APPLICANT: Yi, Minkyung  
 ; TITLE OF INVENTION: REPLICATION COMPETENT HEPATITIS C VIRUS AND METHODS OF USE  
 ; FILE REFERENCE: 265.0007 0121  
 ; CURRENT APPLICATION NUMBER: US/11/006,313  
 ; CURRENT FILING DATE: 2004-12-06  
 ; PRIOR APPLICATION NUMBER: US 60/171,909  
 ; PRIOR FILING DATE: 1999-12-23  
 ; PRIOR APPLICATION NUMBER: US 10/259,275  
 ; PRIOR FILING DATE: 2002-09-27  
 ; PRIOR APPLICATION NUMBER: US 09/747,419  
 ; PRIOR FILING DATE: 2000-12-23  
 ; PRIOR APPLICATION NUMBER: US 60/325,236  
 ; PRIOR FILING DATE: 2001-09-27  
 ; PRIOR APPLICATION NUMBER: US 60/338,123  
 ; PRIOR FILING DATE: 2001-11-13  
 ; NUMBER OF SEQ ID NOS: 73  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 35  
 ; LENGTH: 341  
 ; TYPE: DNA  
 ; ORGANISM: ARTIFICIAL  
 ; FEATURE:  
 ; OTHER INFORMATION: nucleotide sequence of 5' NTR  
 US-11-006-313-35

Query Match 98.1%; Score 20.6; DB 10; Length 341;  
 Best Local Similarity 95.2%; Pred. No. 1;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21  
 DB 43 CCTGTGAGGAAGTCTGTCT 63

Search completed: January 27, 2006, 07:20:37  
 Job time : 349.5 secs

**This Page Blank (uspo)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 27, 2006, 04:38:14 ; Search time 1554.5 Seconds  
(without alignments)  
632.055 Million cell updates/sec

Title: US-10-070-415A-37\_COPY\_410\_430

Perfect score: 21  
Sequence: 1 gcaagtgcgtaggtgcgggg 21

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

EST.\*

1: gb\_est1.\*

2: gb\_est2.\*

3: gb\_est3.\*

4: gb\_hic.\*

5: gb\_est4.\*

6: gb\_est5.\*

7: gb\_est6.\*

8: gb\_est7.\*

9: gb\_gssi.\*

10: gb\_gss2.\*

11: gb\_gss3.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19.4	92.4	516	6	CB151486 K-EST0208
2	18.4	87.6	203	8	DR440487 EST149_06
3	17.8	84.8	407	2	BF551560 UI-R-CO-1
4	17.8	84.8	506	1	AJ648930
5	17.8	84.8	506	1	AJ648952
6	17.8	84.8	530	2	BG664562 DRABFD10
7	17.8	84.8	559	5	BU994237 X004H10_P
8	17.8	84.8	563	1	AW916775
9	17.8	84.8	567	8	CX038861
10	17.8	84.8	586	8	CX254668 1307434_N
11	17.8	84.8	624	8	CX031013
12	17.8	84.8	654	2	BI277038 UI-R-CYO-
13	17.8	84.8	678	8	CX042369
14	17.8	84.8	682	3	BQ200617 UI-R-DZ1-
15	17.8	84.8	1080	3	BM912000
16	17.4	82.9	488	9	BZ250187 CH230-363
17	17.4	82.9	898	3	BI910088
18	17.8	81.0	529	2	BE235677 143244_MA
19	17.8	81.0	535	1	AJ659206
20	17.8	81.0	569	7	CN294880
21	17.8	81.0	574	3	BP455885
22	17.8	81.0	581	3	BP285205

C 96 16.8 80.0 979 6 CA029254  
 97 16.8 80.0 980 11 CN506X0B  
 98 16.8 80.0 1066 2 BE561930  
 99 16.8 80.0 1192 2 BF203712  
 100 16.8 80.0 1250 10 CL081883

ALIGNMENTS

RESULT 1  
 CB151486  
 LOCUS  
 DEFINITION K-EST0208381 C15NU17 Homo sapiens cDNA clone C15NU17-33-C08 5', mRNA sequence.  
 EST 29-JAN-2003  
 ACCESSION CB151486  
 VERSION CB151486.1 GI:28135814  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 516)  
 AUTHORS Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.  
 TITLE 21C Frontier Korean EST Project 2001  
 JOURNAL Unpublished (2002)  
 COMMENT Genome Research Center  
 Korea Research Institute of Bioscience & Biotechnology  
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
 Tel: +82-42-860-4470  
 Fax: +82-42-860-4409  
 Email: yongsung@mail.kribb.re.kr  
 Plate: 33 row: C column: 08  
 High quality sequence stop: 516.  
 Location/Qualifiers  
 1. 516  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="C15NU17-33-C08"  
 /sex="F"  
 /tissue\_type="Uterine"  
 /cell\_type="Epithelial"  
 /cell\_line="SNU-17"  
 /lab\_host="C15NU17"  
 /clone\_lib="C15NU17"  
 /note="Organ: Cervix; Vector: pCNS-D2; Site 1: EcoRI; Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including strand cDNA was synthesized from oligo dt-selected mRNA by ECKRI site by treatment of T4 RNA ligase and the first priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of ECKRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

FEATURES  
 source  
 1. 516  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="C15NU17-33-C08"  
 /sex="F"  
 /tissue\_type="Uterine"  
 /cell\_type="Epithelial"  
 /cell\_line="SNU-17"  
 /lab\_host="C15NU17"  
 /clone\_lib="C15NU17"  
 /note="Organ: Cervix; Vector: pCNS-D2; Site 1: EcoRI; Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including strand cDNA was synthesized from oligo dt-selected mRNA by ECKRI site by treatment of T4 RNA ligase and the first priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of ECKRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 92.4%; Score 19.4; DB 6; Length 516;  
 Best Local Similarity 95.2%; Pred. No. 2.2e+02;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 GCAAGTGTGTAGTGGGG 21

Db

RESULT 2  
 DR440487/c

LOCUS  
 DEFINITION

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS  
 TITLE

JOURNAL  
 PUBMED  
 COMMENT

FEATURES  
 source

1. 203  
 /organism="Phytophthora parasitica"  
 /mol\_type="mRNA"  
 /strain="149"  
 /db\_xref="taxon:4792"  
 /clone="EST149\_06\_D12"  
 /tissue\_type="In vitro grown mycelium"  
 /dev\_stage="4 day old"  
 /lab\_host="VS257"  
 /clone\_lib="myc-149"  
 /note="Vector: pBK-CNV; Site\_1: EcoRI; Site\_2: XhoI;  
 Sample name: 1 experimental condition: rmi medium"

ORIGIN

Query Match 87.6%; Score 18.4; DB 8; Length 203;  
 Best Local Similarity 95.0%; Pred. No. 6.1e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CAAGTGTGTAGTGGGG 21

Db 104 CAAGTGTGTAGTGGGG 85

RESULT 3  
 BF551560/c

LOCUS  
 DEFINITION

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS  
 TITLE

1 (bases 1 to 407)  
 Bonaldo, M.F., Lennon, G. and Soares, M.B.  
 Normalization and subtraction: two approaches to facilitate gene

EST.  
 BF551560.1 GI:11661290  
 EST.  
 Rattus norvegicus (Norway rat)  
 Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridae; Murinae; Rattus.  
 1 (bases 1 to 407)  
 Bonaldo, M.F., Lennon, G. and Soares, M.B.  
 Normalization and subtraction: two approaches to facilitate gene

63 GCAAGTGTGTAGTGGGG 83

DR440487  
 EST149\_06\_D12\_T3 myc-149 Phytophthora parasitica cDNA clone

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS  
 TITLE

JOURNAL  
 PUBMED  
 COMMENT

FEATURES  
 source

1. 203  
 /organism="Phytophthora parasitica"  
 /mol\_type="mRNA"  
 /strain="149"  
 /db\_xref="taxon:4792"  
 /clone="EST149\_06\_D12"  
 /tissue\_type="In vitro grown mycelium"  
 /dev\_stage="4 day old"  
 /lab\_host="VS257"  
 /clone\_lib="myc-149"  
 /note="Vector: pBK-CNV; Site\_1: EcoRI; Site\_2: XhoI;  
 Sample name: 1 experimental condition: rmi medium"

ORIGIN

Query Match 87.6%; Score 18.4; DB 8; Length 203;  
 Best Local Similarity 95.0%; Pred. No. 6.1e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CAAGTGTGTAGTGGGG 21

Db 104 CAAGTGTGTAGTGGGG 85

RESULT 3  
 BF551560/c

LOCUS  
 DEFINITION

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS  
 TITLE

1 (bases 1 to 407)  
 Bonaldo, M.F., Lennon, G. and Soares, M.B.  
 Normalization and subtraction: two approaches to facilitate gene

EST.  
 BF551560.1 GI:11661290  
 EST.  
 Rattus norvegicus (Norway rat)  
 Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridae; Murinae; Rattus.  
 1 (bases 1 to 407)  
 Bonaldo, M.F., Lennon, G. and Soares, M.B.  
 Normalization and subtraction: two approaches to facilitate gene



```

/clone="C0003271_B18"
/tissue type="ovary"
/clone_lib="CSEQRAN19"
/notes="Vector: pBlueScript11(KS+); Site 1: ECORI; Site 2:
NotI; Single pass sequencing; Normalised library
constructed from pooled ovaries"

ORIGIN
Query Match      84.8%; Score 17.8; DB 1; Length 506;
Best Local Similarity 90.5%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTCTGTAGTGGGG 21
|||||
61 GCAAGTCTGTAGTGGTGTG 41

RESULT 6
BG664562/c
LOCUS      530 bp mRNA linear EST 30-APR-2001
DEFINITION DRABFD10 Rat DRG Library Rattus norvegicus cDNA clone DRABFD10 5',
mRNA sequence.
ACCESSION  BG664562
VERSION     BG664562.1 GI:13886484
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
ORGANISM    Rattus norvegicus
REFERENCE    Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
              Sciurognathi; Murioidea; Muridae; Murinae; Rattus.
1 (bases 1 to 530)
Xiao,H.S., Huang,Q.H., Zhang,F.X., Bao,L., Lu,Y.J., Guo,C.,
Yang,L., Huang,W.J., Fu,G., Xu,S.H., Cheng,X.P., Yan,Q., Zhu,Z.D.,
Zhang,X., Chen,Z., Han,Z.G. and Zhang,X.
Identification of gene expression profile of dorsal root ganglion
in the rat peripheral axotomy model of neuropathic pain
Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)
12060780
Contact: Zhang Xu
Laboratory of Sensory System
Institute of Neuroscience
320 Yue Yang Road, Shanghai 200031, P.R.China
Tel: 86-21-64748700-121
Fax: 86-21-64713446
Email: xu.zhang@ion.ac.cn
This clone is also available at Chinese National Human Genome
Center at Shanghai, 351 Guo Shoujing Road, Zhanjiang Hi-Tech Park,
Pudong New Area, P.R.China. Please contact with Zhang Xu
(xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@chgc.sh.cn)
PCR Primers
FORWARD: T3
BACKWARD: T7
Seq primer: T3
POLYA=No.

FEATURES
source      Location/Qualifiers
1..530
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="DRABFD10"
/sex="male"
/tissue type="dorsal root ganglion"
/dev stage="adult"
/clone_lib="Rat DRG Library"

ORIGIN
Query Match      84.8%; Score 17.8; DB 2; Length 530;
Best Local Similarity 90.5%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTCTGTAGTGGGG 21
|||||

```

```

Db      85 GCAAGTCTGTAGTGGTGTG 65

RESULT 7
BUB94237
LOCUS      559 bp mRNA linear EST 17-OCT-2002
DEFINITION X004H10 Populus wood cDNA library Populus tremula x Populus
tremuloides cDNA 5 prime, mRNA sequence.
ACCESSION  BUB94237
VERSION     BUB94237.1 GI:24105302
KEYWORDS    EST.
SOURCE      Populus tremula x Populus tremuloides
ORGANISM    Populus tremula x Populus tremuloides
REFERENCE    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
              rosids; eurosids I; Malpighiales; Salicaceae; Populus.
1 (bases 1 to 559)
Unneberg,P., Bhalerao,R.R., Jansson,S. and Sterky,F.
The poplar tree transcriptome: Analysis of expressed sequence tags
from multiple libraries
Unpublished (2002)
Contact: BHALERAO RUPALI R.
Umea Plant Science Center
Department of Plant Physiology
University of Umea, 901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 6676
Email: rupali.bhalerao@plantphys.umu.se.

FEATURES
source      Location/Qualifiers
1..559
/organism="Populus tremula x Populus tremuloides"
/mol_type="mRNA"
/db_xref="taxon:47664"
/tissue type="wood"
/clone_lib="Populus wood cDNA library"

ORIGIN
Query Match      84.8%; Score 17.8; DB 5; Length 559;
Best Local Similarity 90.5%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTCTGTAGTGGGG 21
|||||
465 GCAAGTGTGAGAGTGGGG 485

Db      465 GCAAGTGTGAGAGTGGGG 485

RESULT 8
AW916775/c
LOCUS      563 bp mRNA linear EST 25-MAY-2000
DEFINITION EST348183 Rat gene index, normalized rat, norvegicus, Bento Soares
Rattus norvegicus cDNA clone RG1DW15 5' end, mRNA sequence.
ACCESSION  AW916775
VERSION     AW916775.1 GI:8082615
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
ORGANISM    Rattus norvegicus
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
              Sciurognathi; Muroidae; Muridae; Murinae; Rattus.
1 (bases 1 to 563)
Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (RST) Catalog & Rat
Gene Index
Unpublished (1998)
Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
This clone is available through the ATCC, contact the ATCC
tel#703-365-2700 for further information

```



```

FEATURES
  source
Seq primer: M13 Reverse.
  Location/Qualifiers
    1..563
      /organism="Rattus norvegicus"
      /mol_type="mRNA"
      /db_xref="taxon:10116"
      /clone="RG1BW15"
      /tissue_type="mix - brain, ovary, placenta, kidney, lung,
      liver, embryo, heart, muscle, spleen"
      /lab_host="SOLR"
      /clone_lib="Rat gene index, normalized rat, norvegicus,
      Bento Soares"
      /note="Vector: pBlueScript SK(-); Site_1: EcoRI; Site_2:
      XhoI; Estimated insert size approx.1 kb"

ORIGIN
Query Match      84.8%; Score 17.8; DB 1; Length 563;
Best Local Similarity 90.5%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGTGGGG 21
    |||||
Db 72 GCAAGTGTCTAGTGTGG 52

RESULT 9
LOCUS CX038861/c
DEFINITION 1351947 NCCWA 10RT#3 Oncorhynchus mykiss cDNA 5', mRNA sequence.
ACCESSION CX038861
VERSION CX038861.1 GI:56983215
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Actinopterygii; Neopterygii; Teleostei; Euteleostei;
  Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE
  Yao,J., Gahr,S. and Rexroad,C.E.
  10RT#3 egg, NCCWA/WVU EST Project, Phase II
  Unpublished (2004)
  Contact: Rexroad CE
  USDA, ARS, National Center for Cool and Cold Water Aquaculture
  11876 Leetown Road, Kearneysville, WV 25430, USA
  Tel: 304 724 8340 x2129
  Fax: 304 725 0351
  Email: crexroad@nccwa.ars.usda.gov
  Single pass sequencing. Bases called with phred v0.020425.c and
  trimmed with the aid of the trim_alt option. Vector identified with
  cross_match v0.990329.
  Plate: 143 row: P column: 9
  Seq primer: GTAATACGACTCACTATAGG.
  Location/Qualifiers
    1..567
      /organism="Oncorhynchus mykiss"
      /mol_type="mRNA"
      /db_xref="taxon:8022"
      /lab_host="DH10B"
      /clone_lib="NCCWA 10RT#3"
      /note="Vector: PCMV Sport6.0; WVU oocyte library RT-EGG."

ORIGIN
Query Match      84.8%; Score 17.8; DB 8; Length 567;
Best Local Similarity 90.5%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGTGGGG 21
    |||||
Db 40 GCTAGGGCTGTAGTGTGGG 20

RESULT 10
LOCUS CX254668
DEFINITION 1307434 NCCWA 02RT Oncorhynchus mykiss cDNA 3', mRNA sequence.
ACCESSION CX254668
VERSION CX254668.1 GI:60371200
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Actinopterygii; Neopterygii; Teleostei; Euteleostei;
  Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE
  Rexroad,C.E., Goupil,A.-S., Guiguen,Y. and Yao,J.
  02RT IUS, NCCWA/WVU EST Project, Phase II, in collaboration with
  INRA
  Unpublished (2004)
  Contact: Rexroad CE
  USDA, ARS, National Center for Cool and Cold Water Aquaculture
  11876 Leetown Road, Kearneysville, WV 25430, USA
  Tel: 304 724 8340 x2129
  Fax: 304 725 0351
  Email: crexroad@nccwa.ars.usda.gov
  Single pass sequencing. Bases called with phred v0.020425.c and
  trimmed with the aid of the trim_alt option. Vector identified with
  cross_match v0.990329.
  Plate: 115 row: K column: 15
  Seq primer: GTAATACGACTCACTATAGG.
  Location/Qualifiers
    1..586
      /organism="Oncorhynchus mykiss"
      /mol_type="mRNA"
      /db_xref="taxon:8022"
      /tissue_type="pooled"
      /lab_host="DH10B"
      /clone_lib="NCCWA 02RT"
      /note="Vector: PCMV Sport6.0; This library was created by
      A.-S. Goupil and Y. Guiguen who substracted the NCCWA 1RT
      library from the INRA multi-tissue library."

ORIGIN
Query Match      84.8%; Score 17.8; DB 8; Length 586;
Best Local Similarity 90.5%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGTGGGG 21
    |||||
Db 530 GCTAGGGCTGTAGTGTGGGG 550

RESULT 11
LOCUS CX031013/c
DEFINITION 1343080 NCCWA 10RT#3 Oncorhynchus mykiss cDNA 5', mRNA sequence.
ACCESSION CX031013
VERSION CX031013.1 GI:56975367
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Actinopterygii; Neopterygii; Teleostei; Euteleostei;
  Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE
  Yao,J., Gahr,S. and Rexroad,C.E.
  10RT#3 egg, NCCWA/WVU EST Project, Phase II
  Unpublished (2004)
  Contact: Rexroad CE
  USDA, ARS, National Center for Cool and Cold Water Aquaculture
  11876 Leetown Road, Kearneysville, WV 25430, USA
  Tel: 304 724 8340 x2129
  Fax: 304 725 0351
  Email: crexroad@nccwa.ars.usda.gov
  Single pass sequencing. Bases called with phred v0.020425.c and
  trimmed with the aid of the trim_alt option. Vector identified with
  cross_match v0.990329.

```

FEATURES	Source
Plate: 119 row: F column: 22	
seq primer: GTAATACGACTCACTATAGG.	
Location/Qualifiers	
1..624	
Accession: "GCA006036.1" model: "1"	

```

/organism="Oncomyrinus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/lab_host="DH10B"
/clone_lib="NCCWA 10RT#3"
/note="Vector: pCWV Sport6.0; WVU oocyte library RT-EGG."

```

ORIGIN

Query Match	84.8%	Score 17.8;	DB 8;	Length 624;
Best Local Similarity	90.5%;	Pred. No. 1.3e+03;		
Method	10. Conservative	0. Mismatches	2. Indels	0. Gaps

Matches	157	Conservative	0	Nonconservative	27	Indels	0	GC%
QY	1	GCAAGTGTGTAGTTCGGGG	21					
Db	374	GCTAGGGCTGTAGTTCGGGG	354					

RESULT 12	BI277038	654 bp	linear	EST 19-JUL-2000
LOCUS	UI-R-CYO-bxp-g-02-0-UI.s1		UI-R-CYO	Rattus norvegicus cDNA clone
DEFINITION	UI-R-CYO-bxp-g-02-0-UI 3', mRNA sequence.			
ACCESSION	BI277038			

VERSION	B1277038.1	GI:14922529
KEYWORDS		
SOURCE		
ORGANISM		
		Rattus norvegicus (Norway rat)
		Rattus norvegicus
		Rattus norvegicus
		Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
		Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
		Sciurognathi; Muridea; Muridae; Murinae; Rattus.

REFERENCE	I (bases 1 to 634)
AUTHORS	Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE	Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL	Genome Res. 6 (9), 791-806 (1996)
PUBMED	8889548
COMMENT	Contact: Soares, MB Coordinated Laboratory for Computational Genomics

University of Iowa  
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: bento-boares@uiowa.edu

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence was present in the cDNA between the NotI site

tail. The sequence tag presented in the Genbank database (U01111) and the oligo-dT track served to verify it as a clone from the non-normalized brown adipose library cDNA library Preparation: M.E. Soares Lab Clone distribution: clones will be available through Research Genetics ([www.resgen.com](http://www.resgen.com)).

```

FEATURES
  source
    Location/Qualifiers
      seq primer: M13 forward
      POLYA=Yes.
      1. .654
      /organism="Rattus norvegicus"

```

```

/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-CY0-bxp-g-02-0-UI"
/dev_stage="ADULT"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-CY0"

```

/note="Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; The UI-R-CY0 library is a non-normalized library constructed from rat brown adipose tissue. For a detailed description of the library from which this clone was derived, please visit [www.scripps.edu](http://www.scripps.edu). The subtraction hybridization site at rat.scripps.edu.

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Rattus.

## REFERENCE

1 (bases 1 to 682)  
Bonaldo, M.F., Lennon, G. and Soares, M.B.  
Normalization and subraction: two approaches to facilitate gene  
discovery

## JOURNAL

Genome Res. 6 (9), 791-806 (1996)

## PUBMED

8889548

## COMMENT

Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgapbs-r@mail.nih.gov

Oligo-dr track not found, Not I site shown in beginning of sequence  
is likely internal to the message. cDNA Library Preparation: M.B.  
Soares Lab Clone distribution: clones will be available through  
IMAGE (<http://image.llnl.gov>)

Seq primer: M13 Forward

POLYA=Yes.

## FEATURES

Location/Qualifiers

1..682

/organism="Rattus norvegicus"

/mol\_type="mRNA"

/strain="Sprague-Dawley"

/db\_xref="taxon:10116"

/clone="IMAGE:7344618"

/tissue\_type="Chondrosarcoma"

/dev\_stage="37 days"

/lab\_host="DH10B (Life Technologies)"

/clone\_lib="NCI CGAP\_D21"

/note="Organ: Spine; Vector: p7T3D-Pac (Pharmacia) with a  
modified polylinker; Site 1: Not I; Site 2: Eco RI;  
UI-R-D21 is a normalized cDNA library containing the  
following tissue(s): Swarm Rat Chondrosarcoma. The library  
was constructed according to Bonaldo, Lennon and Soares,  
Genome Research, 6:791-806, 1996. First strand cDNA  
synthesis was primed with an oligo-dr primer containing a  
Not I site. Double stranded cDNA was ligated to an EcoR I  
adaptor, digested with Not I, and cloned directionally  
into p7T3-Pac vector. The oligonucleotide used to prime  
the synthesis of first-strand cDNA contains a library tag  
sequence that is located between the Not I site and the  
(dT)18 tail. The sequence tag for this library is  
CATCTTGTA. The Rat cartilaginous tumor tissue was  
provided by Dr Jeff Stevens at the University of Iowa.  
TAG TISSUE=cartilaginous tumor  
TAG\_LIB=UI-R-D21  
TAG\_SEQ=CATCTTGTA"

## ORIGIN

Query Match

Best Local Similarity 84.8%; Score 17.8; DB 3; Length 682;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCTGTAGTGGCGGG 21

|||||

Db 608 GCAAGTCTGTAGTGGCTGTG 628

## RESULT 15

BM912000/c

## LOCUS

AGENCY 6613112 NIH\_MGC\_41 Homo sapiens cDNA clone IMAGE:5473480

5', mRNA sequence.

## ACCESSION

BM912000

## VERSION

BM912000.1

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 1080)

## AUTHORS

TITLE

JOURNAL

COMMENT

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DRP

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: L1CM1985 row: c column: 17

High quality sequence stop: 531.

Location/Qualifiers

source

1..1080

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5473480"

/tissue\_type="amelanotic melanoma, cell line"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH MGC\_41"

/note="Organ: skin; Vector: pOTF7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dr priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GGCAGGAG(G). Library constructed by Ling Hong in the

laboratory of Gerald M. Rubin (University of California,

Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

Superscript II RT (Life Technologies). Note: this is a

NIH\_MGC Library."

## ORIGIN

Query Match

Best Local Similarity 84.8%; Score 17.8; DB 3; Length 1080;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCTGTAGTGGCGGG 21

|||||

Db 711 GCAATTGCTGTGGTGGCGGG 691

## RESULT 16

BZ250187

## LOCUS

CH230-363D18 TV CHORI-230 Segment 2 Rattus norvegicus genomic clone

CH230-363D18, genomic survey sequence.

BZ250187 488 bp DNA linear GSS 12-OCT-2002

CH230-363D18, genomic survey sequence.

BZ250187 488 bp DNA linear GSS 12-OCT-2002

CH230-363D18, genomic survey sequence.

BZ250187 488 bp DNA linear GSS 12-OCT-2002

CH230-363D18, genomic survey sequence.

BZ250187 488 bp DNA linear GSS 12-OCT-2002

CH230-363D18, genomic survey sequence.

BZ250187 488 bp DNA linear GSS 12-OCT-2002

CH230-363D18, genomic survey sequence.

BZ250187 488 bp DNA linear GSS 12-OCT-2002

CH230-363D18, genomic survey sequence.

BZ250187 488 bp DNA linear GSS 12-OCT-2002

CH230-363D18, genomic survey sequence.

BZ250187 488 bp DNA linear GSS 12-OCT-2002

CH230-363D18, genomic survey sequence.

BZ250187 488 bp DNA linear GSS 12-OCT-2002

CH230-363D18, genomic survey sequence.

BZ250187 488 bp DNA linear GSS 12-OCT-2002

CH230-363D18, genomic survey sequence.

BZ250187 488 bp DNA linear GSS 12-OCT-2002

CH230-363D18, genomic survey sequence.

BZ250187 488 bp DNA linear GSS 12-OCT-2002

CH230-363D18, genomic survey sequence.

BZ250187 488 bp DNA linear GSS 12-OCT-2002

CH230-363D18, genomic survey sequence.

BZ250187 488 bp DNA linear GSS 12-OCT-2002

CH230-363D18, genomic survey sequence.

BZ250187 488 bp DNA linear GSS 12-OCT-2002

CH230-363D18, genomic survey sequence.

BZ250187 488 bp DNA linear GSS 12-OCT-2002

CH230-363D18, genomic survey sequence.

(http://www.chori.org/bacpac/or ering information.htm). BAC end  
 page: http://www.tigr.org/tdb/bac\_ends/rat/bac\_end\_intro.html  
 Plate: 363 row: D column: 18  
 Seq primer: F7  
 Class: BAC ends.

FEATURES  
 source  
 Location/Qualifiers  
 1..488  
 /organism="Rattus norvegicus"  
 /mol\_type="genomic DNA"  
 /strain="BN/SsNHsd/MCW"  
 /db\_xref="taxon:10116"  
 /clone="CH230-363D18"  
 /sex="Female"  
 /cell\_type="Brain"  
 /clone\_lib="CHORI-230 Segment 2"  
 /note="Vector: PTARBAC1.3; Site 1: MboI; Site 2: MboI;  
 CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by  
 Pieter de Jong"

## ORIGIN

Query Match 82.9%; Score 17.4; DB 9; Length 488;  
 Best Local Similarity 94.7%; Pred. No. 2e+03;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CAAGTCTGTAGTGGGG 20  
 |||||  
 Db 2 CAAGTCTGTAGTGGGG 20

## RESULT 17

BI910088 898 bp mRNA linear EST 16-OCT-2001  
 LOCUS 603067926F1 NIH\_MGC\_118 Homo sapiens cDNA clone IMAGE:5216958 5',  
 DEFINITION mRNA sequence.

ACCESSION BI910088  
 VERSION BI910088.1 GI:16173428  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

## REFERENCE

1 (bases 1 to 898)  
 NIH-MGC http://mgi.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs@mail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LHAM1545 row: C column: 07  
 High quality sequence stop: 779.

FEATURES  
 source  
 Location/Qualifiers  
 1..898  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5216958"  
 /tissue\_type="leukocyte"  
 /lab\_host="DH10B"  
 /clone\_lib="NIH\_MGC\_118"  
 /note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV  
 (destroyed); RNA source leukocytes from anonymous pool of  
 non-activated adult donors. Library is oligo-dT primed  
 and directionally cloned (EcoRV site is destroyed upon  
 cloning). Average insert size 1.7 kb, insert size range  
 1.2-3.3 kb. Library is normalized and enriched for  
 full-length clones and was constructed by C. Gruber

(Invitrogen). Research Genetics tracking code 027. Note:  
 this is a NIH\_MGC Library."

ORIGIN  
 Query Match 82.9%; Score 17.4; DB 3; Length 898;  
 Best Local Similarity 94.7%; Pred. No. 2.1e+03;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CAAGTCTGTAGTGGGG 20  
 |||||  
 Db 531 CAAGTCTGTAGTGGGG 549

## RESULT 18

BE235677/c 529 bp mRNA linear EST 10-JUL-2000  
 LOCUS 143244 MARC 1P1G Sus scrofa cDNA 5', mRNA sequence.  
 DEFINITION BE235677  
 ACCESSION BE235677  
 VERSION BE235677.1 GI:9020395  
 KEYWORDS EST.

SOURCE Sus scrofa (pig)  
 ORGANISM Sus scrofa  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
 Sus. (bases 1 to 529)

REFERENCE 1 (bases 1 to 529)  
 AUTHORS Fahrkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J.,  
 Vallet,J., Wise,T., Rohrer,G.A., Perlea,G., Sultana,R.,  
 Quackenbush,J. and Keeler,J.W.  
 Porcine gene discovery by normalized cDNA-library sequencing and  
 EST cluster assembly  
 Mamm. Genome 13 (8), 475-478 (2002)

JOURNAL 12226715  
 PUBMED  
 COMMENT Contact: Smith TPL  
 USDA, ARS, US Meat Animal Research Center  
 PO Box 166, Clay Center, NE 68933-0166, USA  
 Tel: 402 762 4366  
 Fax: 402 762 4390

Email: smith@email.marc.usda.gov  
 Single pass sequencing. Bases called and alt\_trimmed with phred  
 v0.980904.e. Vector identified by cross\_match with the -minscore 18  
 and -minmatch 12 options.

PCR Primers  
 FORWARD: AGAAACACGCTATGACCAT  
 BACKWARD: GTTTCACGTCACGACG  
 Plate: 84 row: K column: 8  
 Seq primer: ATTAGTGACACTATAG.

FEATURES  
 source  
 Location/Qualifiers  
 1..529  
 /organism="Sus scrofa"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9823"  
 /tissue\_type="pooled"  
 /lab\_host="DH10B"  
 /clone\_lib="MARC 1P1G"  
 /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;  
 Library made from pooled tissue from day 11, 13, 15, 20,  
 and 30 embryos."

## ORIGIN

Query Match 81.0%; Score 17; DB 2; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGGG 21  
 |||||  
 Db 192 GTGCTGTAGTGGGG 176

## RESULT 19

AJ659206 535 bp mRNA linear EST 28-JUN-2004  
 LOCUS AJ659206 KN277 Sus scrofa cDNA clone C0005215\_I12, mRNA sequence.  
 DEFINITION

```

ACCESSION AJ659206
VERSION AJ659206.1 GI:49343337
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
          Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
          Eukaryota; Metazoa; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
          Suis.

REFERENCE 1 (bases 1 to 535)
AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLE Development of cDNA and EST resources for studying reproduction and
        embryo development in pigs and cattle
JOURNAL Unpublished (2004)
COMMENT Contact: Anderson SI
        Genomics and Bioinformatics
        Roslin Institute
        Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
        Single pass sequencing. Bases called and trimmed with phred
        v0.020425.c. Vector identified by crossmatch with the -minscore 20
        and -minmatch 12 options. Vector:pBlueScriptII(SK+) R. Site1: EcoRI
        R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
        from pooled early embryos, from 8- cell stage to blastocysts.
        Clones available from UK Centre for Functional Genomics in Farm
        Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS,
        www.arkgenomics.org.
FEATURES             Location/Qualifiers
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                     /clone="C0005215_112"
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                     to blastocysts."
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Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGC GGCGG 21
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Db 45 GTGCTGTAGTGC GGCGG 29

RESULT 20
CN294880/c
LOCUS CN294880 569 bp mRNA linear EST 16-MAY-2004
DEFINITION 17000600093822 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN294880
VERSION CN294880.1 GI:47311294
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homnidae; Homo.
          1 (bases 1 to 569)
          Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
          Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
          Lebkowski,J. and Stanton,L.W.
          Transcriptome characterization elucidates signaling networks that
          control human ES cell growth and differentiation
          Nat. Biotechnol. 22 (6), 707-716 (2004)
          15146197
          Contact: Brandenberger R
          Regenerative Medicine
          Genon Corporation
          230 Constitution Drive, Menlo Park, CA 94025, USA
          Tel: 650 473 8658

```

```

Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 569 Std Error: 0.00.
Location/Qualifiers
1..569
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, DMSO-treated H9 cell
line"
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/note="oligo dt primed, full-length enriched cDNA library
from DMSO-treated hES cell line H9 (p22) maintained in
feeder-free conditions"
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Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGC GGCGG 21
    |||||||
Db 548 GTGCTGTAGTGC GGCGG 532

RESULT 21
BP455885/c
LOCUS BP455885 574 bp mRNA linear EST 31-DEC-2003
DEFINITION BP455885 full-length enriched swine cDNA library, adult ovary Sus
          scrofa cDNA clone OVRM10038B05 5', mRNA sequence.
ACCESSION BP455885
VERSION BP455885.1 GI:40467400
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
          Suis.
          1 (bases 1 to 574)
          Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,
          Okumura,N., Hamasima,N. and Awata,T.
          PEDE (pig EST Data Explorer): construction of a database for ESTs
          derived from porcine full-length cDNA libraries
          Nucleic Acids Res. 32 (1), D484-D488 (2004)
          14681463
          Contact: Hirohide Uenishi
          Animal Genome Laboratory, Genome Research Department
          National Institute of Agrobiological Sciences
          2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
          Tel: +81-29-838-8627
          Fax: +81-29-838-8627
          Email: huenishi@affrc.go.jp
          EST project with full-length enriched cDNA libraries carried out in
          Animal Genome Research Program (Japan) by National Institute of
          Agrobiological Sciences and STAFF-Institute
          Single pass sequencing of clones derived from oligo-capped cDNA
          library
          Vector sequences were eliminated by RepeatMasker version 2002/07/13
          and crossmatch version 0.990319
          Low quality bases were trimmed based on the quality values.
FEATURES             Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 3.1e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 17; Conservative 0;

QY 5 GTGCTGTAGTGGGGG 21
Db 574 GTGCTGTAGTGGGGG 558

RESULT 22
BP285205/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT
FEATURES
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1..581
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/cell_type="fibroblast"
/clone_lib="Sugano cDNA library, lung fibroblast"
/note="normal"

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Best Local Similarity 100.0%; Pred. No. 3.1e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 17; Conservative 0;

QY 5 GTGCTGTAGTGGGGG 21
Db 567 GTGCTGTAGTGGGGG 551

RESULT 23
BP288204/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
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REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT
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Query Match 81.0%; Score 17; DB 3; Length 581;
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Matches 17; Conservative 0;

QY 5 GTGCTGTAGTGGGGG 21
Db 574 GTGCTGTAGTGGGGG 558

RESULT 24
BP288316/c
LOCUS
DEFINITION
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VERSION
KEYWORDS
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AUTHORS
TITLE
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Matches 17; Conservative 0;

QY 5 GTGCTGTAGTGGGGG 21
Db 571 GTGCTGTAGTGGGGG 555

RESULT 25
BP288316/c
LOCUS
DEFINITION
ACCESSION
VERSION
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REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT
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Matches 17; Conservative 0;

QY 5 GTGCTGTAGTGGGGG 21
Db 571 GTGCTGTAGTGGGGG 555

```

```

15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.

FEATURES
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/clone_lib="Sugano cDNA library, lung fibroblast"
/note="normal"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3.1e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 17; Conservative 0;

QY 5 GTGCTGTAGTGGGGG 21
Db 568 GTGCTGTAGTGGGGG 552

RESULT 24
BP288316/c
LOCUS
DEFINITION
ACCESSION
VERSION
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REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT
FEATURES
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/organism="Homo sapiens"
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Matches 17; Conservative 0;

QY 5 GTGCTGTAGTGGGGG 21
Db 571 GTGCTGTAGTGGGGG 555

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 582)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
SOURCE
1. 582
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Best Local Similarity 100.0%; Pred. No. 3.1e+03;
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QY 5 GTGCTGTAGTGCGGGG 21
|||||
Db 571 GTGCTGTAGTGCGGGG 555

RESULT 29
BP286331/c
LOCUS
DEFINITION
BP286331 Sugano cDNA library, lung fibroblast Homo sapiens cDNA
clone LFL03946, mRNA sequence.
ACCESSION
BP286331
VERSION
BP286331.1 GI:52200063
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 582)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
SOURCE
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/clone_lib="Sugano cDNA library, lung fibroblast"
/note="normal"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGCGGGG 21
|||||
Db 571 GTGCTGTAGTGCGGGG 555

RESULT 29
BP286331/c
LOCUS
DEFINITION
BP286331 Sugano cDNA library, lung fibroblast Homo sapiens cDNA
clone LFL03946, mRNA sequence.
ACCESSION
BP286331
VERSION
BP286331.1 GI:52200063
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 582)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
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QY 5 GTGCTGTAGTGCGGGG 21
|||||
Db 571 GTGCTGTAGTGCGGGG 555

RESULT 30
BP287184/c
LOCUS
DEFINITION
BP287184 Sugano cDNA library, lung fibroblast Homo sapiens cDNA
clone LFL05920, mRNA sequence.
ACCESSION
BP287184
VERSION
BP287184.1 GI:52200916
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 582)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
SOURCE
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QY 5 GTGCTGTAGTGCGGGG 21
|||||
Db 570 GTGCTGTAGTGCGGGG 554

RESULT 31
BP287610/c
LOCUS
DEFINITION
BP287610 Sugano cDNA library, lung fibroblast Homo sapiens cDNA
clone LFL07025, mRNA sequence.
ACCESSION
BP287610
VERSION
BP287610.1 GI:52201342
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 582)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
SOURCE
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3.1e+03;
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QY 5 GTGCTGTAGTGCGGGG 21
|||||
Db 570 GTGCTGTAGTGCGGGG 554

RESULT 31
BP287610/c
LOCUS
DEFINITION
BP287610 Sugano cDNA library, lung fibroblast Homo sapiens cDNA
clone LFL07025, mRNA sequence.
ACCESSION
BP287610
VERSION
BP287610.1 GI:52201342
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 582)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
SOURCE
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Query Match 81.0%; Score 17; DB 3; Length 582;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGCGGGG 21
|||||
Db 570 GTGCTGTAGTGCGGGG 554
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JOURNAL  
PUBMED  
COMMENT

Genome Res. 14 (9), 1711-1718 (2004)  
15342556  
Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: ysuzuki@ims.u-tokyo.ac.jp.

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## ORIGIN

Query Match 81.0%; Score 17; DB 3; Length 582;  
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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGCGGG 21

Db 545 GTGCTGTAGTGGCGGG 529

## RESULT 32

BP354534/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BP354534 582 bp mRNA linear EST 17-SEP-2004  
clone T7R04243, mRNA sequence.

BP354534

BP354534.1 GI:52284520

EST.

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 582)

Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,

Mizushima-Sugano,J., Nakai,K. and Sugano,S.

Sequence comparison of human and mouse genes reveals a homologous

block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)

15342556

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp.

Location/Qualifiers

1. .582

/organism="Homo sapiens"

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ORIGIN

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QY 5 GTGCTGTAGTGGCGGG 21

Db 573 GTGCTGTAGTGGCGGG 557

## RESULT 33

BP359182/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BP359182 582 bp mRNA linear EST 17-SEP-2004  
clone TDR08082, mRNA sequence.

BP359182

BP359182.1 GI:52289195

EST.

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 582)

Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,

Mizushima-Sugano,J., Nakai,K. and Sugano,S.

Sequence comparison of human and mouse genes reveals a homologous

block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)

15342556

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp.

Location/Qualifiers

1. .582

/organism="Homo sapiens"

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/note="mammary gland tumor"

ORIGIN

Query Match 81.0%; Score 17; DB 3; Length 582;  
Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGCGGG 21

Db 571 GTGCTGTAGTGGCGGG 555

## RESULT 34

BP285644/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BP285644 583 bp mRNA linear EST 16-SEP-2004  
clone LFL02445, mRNA sequence.

BP285644

BP285644.1 GI:52199376

EST.

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 583)

Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,

Mizushima-Sugano,J., Nakai,K. and Sugano,S.

Sequence comparison of human and mouse genes reveals a homologous

block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)

15342556

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp.

Location/Qualifiers

1. .582

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="LFL02445"

/cell\_type="mammary gland"

/cell\_line="T47D"

/clone\_lib="Sugano cDNA library, mammary gland T47D"

/note="mammary gland tumor"

ORIGIN

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source
1. .583
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="LFL02445"
/tissue_type="lung"
/cell_type="fibroblast"
/clone_lib="Sugano cDNA library, lung fibroblast"
/notes="normal"

ORIGIN
Query Match      81.0%; Score 17; DB 3; Length 583;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  5 GTGCTGTAGTGGCGGG 21
      |||||
Db  570 GTGCTGTAGTGGCGGG 554

RESULT 35
BP286330/c
LOCUS
DEFINITION
BP286330 Sugano cDNA library, lung fibroblast Homo sapiens CDNA
clone LFL03941, mRNA sequence.
ACCESSION
BP286330
VERSION
BP286330.1 GI:52200062
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
1 (bases 1 to 583)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

AUTHORS
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

TITLE
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL
Genome Res. 14 (9), 1711-1718 (2004)
PUBMED
15342556
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
source
1. .583
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="LFL03941"
/tissue_type="lung"
/cell_type="fibroblast"
/clone_lib="Sugano cDNA library, lung fibroblast"
/notes="normal"

ORIGIN
Query Match      81.0%; Score 17; DB 3; Length 583;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  5 GTGCTGTAGTGGCGGG 21
      |||||
Db  571 GTGCTGTAGTGGCGGG 555

RESULT 36
BP287530/c
LOCUS
DEFINITION
BP287530 Sugano cDNA library, lung fibroblast Homo sapiens CDNA
clone LFL06826, mRNA sequence.
ACCESSION
BP287530
VERSION
BP287530.1 GI:52201262

```

```

KEYWORDS
SOURCE
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
1 (bases 1 to 583)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
source
1. .583
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="LFL06826"
/tissue_type="lung"
/cell_type="fibroblast"
/clone_lib="Sugano cDNA library, lung fibroblast"
/notes="normal"

ORIGIN
Query Match      81.0%; Score 17; DB 3; Length 583;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  5 GTGCTGTAGTGGCGGG 21
      |||||
Db  572 GTGCTGTAGTGGCGGG 556

RESULT 37
BP342212/c
LOCUS
DEFINITION
BP342212 Sugano cDNA library, stomach mucosa Homo sapiens cDNA
clone STM04411, mRNA sequence.
ACCESSION
BP342212
VERSION
BP342212.1 GI:52271993
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
1 (bases 1 to 583)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
source
1. .583
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="STM04411"
/tissue_type="stomach mucosa"
/clone_lib="Sugano cDNA library, stomach mucosa"

ORIGIN

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Query Match 81.0%; Score 17; DB 3; Length 583;  
Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGCGGG 21  
|||||  
Db 571 GTGCTGTAGTGGCGGG 555

RESULT 38  
CA406235/c  
LOCUS 1002384 Human Fat Cell 5'-Stretch Plus cDNA Library Homo sapiens EST 07-NOV-2002  
DEFINITION cDNA 5', mRNA sequence.  
ACCESSION CA406235  
VERSION CA406235.1 GI:24771106  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 603)  
Yang, R.-Z., Shuldiner, A. and Gong, D.-W.  
EST analysis of human adipose gene expression  
Unpublished (2002)  
Contact: Gong Da-Wei  
Division of Endocrinology, Diabetes and Nutrition  
University of Maryland  
660 Redwood St., HH497, Baltimore, MD 21201, USA  
Tel: 410 706 1672  
Fax: 410 706 1622  
Email: dgong@medicine.umaryland.edu  
PCR Primers  
FORWARD: CTCGGGAGCGGCCATTGTGTGGT  
BACKWARD: AATAGACTCACTATAGGCGGAATTG  
Seq primer: GTTGGTACCCGGGAATTC.  
Location/Qualifiers  
1. .603  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/sex="Male and Female"  
/tissue\_type="Adipose"  
/clone\_lib="Human Fat Cell 5'-Stretch Plus cDNA Library"  
/note="Vector: lambdaTriplex"

ORIGIN  
Query Match 81.0%; Score 17; DB 3; Length 603;  
Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGCGGG 21  
|||||  
Db 570 GTGCTGTAGTGGCGGG 554

RESULT 40  
AUI28757/c  
LOCUS AUI28757 NT2RP2 Homo sapiens cDNA clone NT2RP2004133 5', mRNA EST 01-AUG-2002  
DEFINITION sequence.  
ACCESSION AUI28757  
VERSION AUI28757.1 GI:10989111  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 633)  
Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,  
Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and  
Isogai, T.  
HRI human cDNA project  
Unpublished (2000)  
Contact: Takao Isogai  
Genomics Laboratory  
Helix Research Institute  
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
Tel: 81-438-52-3975  
Fax: 81-438-52-3986  
Email: genomics@hri.co.jp  
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix  
Research Institute; cDNA library construction: Department of  
Virology, Institute of Medical Science, University of Tokyo, and  
Helix Research Institute.  
Location/Qualifiers  
1. .633  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="NT2RP2004133"  
/cell\_type="teratocarcinoma"  
/cell\_line="NT2"  
/clone\_lib="NT2RP2"  
/note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor  
cells after 2-weeks retinoic acid (RA) induction"

ORIGIN  
Query Match 81.0%; Score 17; DB 6; Length 603;  
Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGCGGG 21  
|||||  
Db 537 GTGCTGTAGTGGCGGG 521

RESULT 39  
BP336613/c  
LOCUS BP336613 Sugano cDNA library, coronary artery smooth muscle cell EST 17-SEP-2004  
DEFINITION Homo sapiens cDNA clone SMR06107, mRNA sequence.  
ACCESSION BP336613  
VERSION BP336613.1 GI:52266194  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 611)  
Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,



Clingsmith, T.R., Hartley, J.L., Esposito, D., Cheo, D., Moore, T., Simmons, B., Sequeira, R., Bosak, S., Doucette-Stamm, L., Le Peuch, C., Vandenhaute, J., Cusick, M.E., Albala, J.S., Hill, D.E. and Vidal, M. Human ORFeome Version 1.1: a Platform for Reverse Proteomics Genome Res. (2004) In press

Contact: Vidal M  
Marc Vidal Laboratory  
Dana Farber Cancer Institute  
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA  
Tel: 617 632 5180  
Fax: 617 632 5739  
Email: Marc.Vidal@dfci.harvard.edu

ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF results from a PCR reaction using an MGC full-length cDNA as template DNA and ORF specific primers

PCR Primers  
FORWARD: ATGGGGGAACACAGTCCAGACAA  
BACKWARD: CACTTGGAGAGCTGCTGGTGA  
Insert Length: 638 Std Error: 41.00  
Plate: 11078 row: 05 column: A  
Seq primer: ACTGGCCGTCGTTTACAAACGTCGTGACTGGGAAAC  
High quality sequence start: 101  
High quality sequence stop: 637  
POLYA=No.

# FEATURES

source

Location/Qualifiers

1..638  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="mixed"  
/clone\_lib="Full length cDNA from the Mammalian Gene Collection"

/note="Vector: mixed; The ORFs were PCR amplified from the MGC (Mammalian Gene Collection) as of April 2004 and cloned by recombinational Gateway cloning into pDONR223 Donor vector. Reference : MGC (Mammalian Gene Collection) Program Team, Generation and Initial Analysis of more than 15,000 Full-Length Human and Mouse cDNA Sequences. PNAS, 2002, 99(26), 16899-16903"

# ORIGIN

Query Match 81.0%; Score 17; DB 7; Length 638;  
Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGCGGG 21  
|||||

Db 458 GTGCTGTAGTGGCGGG 442  
|||||

# RESULT 44

BW967847/c

LOCUS

DEFINITION BW967847 full-length enriched swine cDNA library, adult ovary Sus scrofa cDNA clone OVR010096F06 5', mRNA sequence.

ACCESSION BW967847

VERSION BW967847

KEYWORDS EST.

SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.

# REFERENCE

AUTHORS

1 (bases 1 to 716)  
Unishi, H., Eguchi, T., Suzuki, K., Sawazaki, T., Toki, D., Shinkai, H., Okumura, N., Hamashima, N. and Awata, T.

TITLE

PEDE (Pig EST Data Explorer): construction of a database for ESTs derived from porcine full-length cDNA libraries

JOURNAL

PUBLISHED Nucleic Acids Res. 32 (1), D484-D488 (2004)

COMMENT

14681463  
Contact: Hirohide Unishi  
Animal Genome Laboratory, Genome Research Department  
National Institute of Agrobiological Sciences

2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan

Tel: +81-29-838-8627

Fax: +81-29-838-8627

Email: huenishi@affrc.go.jp

EST project with full-length enriched cDNA libraries carried out in Animal Genome Research Program (Japan) by National Institute of Agrobiological Sciences and STAFF-Institute  
Single pass sequencing of clones derived from oligo-capped cDNA library

Vector sequences were eliminated by RepeatMasker version 2002/07/13 and crossmatch version 0.990319

Low quality bases were trimmed based on the quality values.

# FEATURES

source

Location/Qualifiers

1..716  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone="OVR010096F06"  
/tissue\_type="ovary"  
/dev\_stage="adult"  
/clone\_lib="full-length enriched swine cDNA library, adult ovary"

# ORIGIN

Query Match 81.0%; Score 17; DB 5; Length 716;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGCGGG 21  
|||||

Db 594 GTGCTGTAGTGGCGGG 578  
|||||

# RESULT 45

DN994620/c

LOCUS

DEFINITION DN994620 Human adult whole brain, large insert, pCMV expression library Homo sapiens cDNA clone TC116396 5', similar to Homo sapiens metal-regulatory transcription factor 1 (MTF1), mRNA sequence.

ACCESSION DN994620

VERSION DN994620.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

# REFERENCE

AUTHORS

1 (bases 1 to 722)  
Birkett, C., Cho, J., Gau, Y., Hamer, R., Kelly, S., Kovacs, K., Liu, L., Liu, X., Porter, J., Sachs, A., Shu, Y., Sun, Z., Wong, J., Wu, M., Zhang, X., Jay, G. and He, W.

TITLE

High-throughput cloning of full-length human cDNAs directly from cDNA libraries optimized for large and rare transcripts  
Unpublished (2005)  
Contact: Kovacs, KF

JOURNAL

COMMENT

High Throughput cDNA Cloning  
Origene Technologies, Inc. (www.origene.com)

6 Taft Court, Suite 100, Rockville, MD 20850, USA  
Tel: 301 340 3188  
Fax: 301 340 8606

Email: cDNA@origene.com

This EST submission is part of an on-going human full-length cloning project at Origene Technologies, Inc.  
Please contact Origene for access.

Origene Technologies, Inc.  
6 Taft Ct. Suite 100  
Rockville, MD 20850

Tel: (301) 340-3188  
http://www.origene.com

Seq primer: pCMV6 5prime forward vector primer, Origene Technologies Inc.

Location/Qualifiers

1..722

# FEATURES

source

Location/Qualifiers

1..722

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="TC116396"  
/tissue\_type="Whole brain"  
/clone\_lib="Human adult whole brain, large insert, PCMV  
expression library"  
/note="Organ: Brain; Vector: pCMV6-XL5; Site 1: EcoRI;  
Site 2: XhoI/SalI compatible end ligation; Oligo-dT primed  
reverse transcription optimized for large and GC rich mRNA  
transcripts, cDNA size selection, optimized ligation for  
large inserts into mammalian expression vector, random  
clones selected for end sequence verification of  
full-length genes"

ORIGIN

Query Match 81.0%; Score 17; DB 8; Length 722;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGCGGG 21  
|||||

Db 565 GTGCTGTAGTGGCGGG 549  
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RESULT 46  
AL702908/c  
LOCUS  
DEFINITION DKFZp686F0317\_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone  
ACCESSION DKFZp686F0317 5', mRNA sequence.  
VERSION AL702908  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 755)  
AUTHORS Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and  
Wiemann, S.  
TITLE EST (Duesterhoeft, et al.)  
JOURNAL Unpublished (1999)  
COMMENT Contact: MIPS  
MIPS  
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing  
consortium of the German Genome Project.  
No sl sequence available.  
This clone (DKFZp686F0317) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.  
Location/Qualifiers  
1..755  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DKFZp686F0317"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="686 (synonym: hlcc3)"  
/note="Vector: pTriplex2; Site\_1: SfiIA; Site\_2: SfiIB;  
cDNA-collection"

ORIGIN

Query Match 81.0%; Score 17; DB 1; Length 755;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGCGGG 21  
|||||

Db 600 GTGCTGTAGTGGCGGG 584  
|||||

RESULT 47  
BU500524/c  
LOCUS  
DEFINITION BU500524 889 bp mRNA linear EST 12-SEP-2002  
AGENCOURT\_7860803 NIH\_MGC\_64 Homo sapiens cDNA clone IMAGE:6109541  
5', mRNA sequence.  
ACCESSION BU500524  
VERSION BU500524.1 GI:22801559  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 889)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: NIMH/LOQ  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LCM2355 row: j column: 06  
High quality sequence start: 3  
High quality sequence stop: 707.  
Location/Qualifiers  
1..889  
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/db\_xref="taxon:9606"  
/clone="IMAGE:6109541"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 64"  
/note="Vector: pOT7a; Site 1: CeuI; Site 2: SceI; This  
library is a size selection of NIH\_MGC\_35\_ from 3.0-4.5  
kb. Size selection done at the National Institute of  
Mental Health, NIH. Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 81.0%; Score 17; DB 5; Length 889;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGCGGG 21  
|||||

Db 571 GTGCTGTAGTGGCGGG 555  
|||||

RESULT 48  
BI257931/c  
LOCUS  
DEFINITION BI257931 939 bp mRNA linear EST 17-JUL-2001  
602970872F1 NIH\_MGC\_12 Homo sapiens cDNA clone IMAGE:5110505 5',  
mRNA sequence.  
ACCESSION BI257931  
VERSION BI257931.1 GI:14813786  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 939)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)

## COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs@mail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: Incyte Genomics, Inc.  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Plate: LLAM11267 row: o column: 18  
 High quality sequence stop: 816.  
 Location/Qualifiers  
 1..939

## FEATURES

source  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5110505"  
 /tissue\_type="cervical carcinoma cell line"  
 /lab\_host="DH10B"  
 /clone\_lib="NIH MGC 12"  
 /note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.4 kb. Library prepared by Life Technologies."

## ORIGIN

Query Match 81.0%; Score 17; DB 2; Length 939;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGGGG 21  
 |||||

DB 92 GTGCTGTAGTGGGGG 76  
 |||||

## RESULT 49

## BE796390/c

LOCUS BE796390 960 bp mRNA linear EST 20-SEP-2000  
 DEFINITION 601592115F1 NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:3946178 5', mRNA sequence.

ACCESSION BE796390  
 VERSION BE796390.1 GI:10217588

KEYWORDS EST.

SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.

REFERENCE 1 (bases 1 to 960)

AUTHORS NIH-MGC <http://mgc.mci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: DCTD/DTF

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: [image.llnl.gov](http://image.llnl.gov)

Plate: LLC805 row: n column: 03

High quality sequence stop: 706.

Location/Qualifiers

1..960

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3946178"

/tissue\_type="small cell carcinoma"

/cell\_line="MGC3"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_7"

/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:

## ORIGIN

Query Match 81.0%; Score 17; DB 2; Length 960;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGGGG 21  
 |||||

DB 521 GTGCTGTAGTGGGGG 505  
 |||||

## RESULT 50

## DQ052866/c

## LOCUS

DQ052866 1831 bp DNA linear GSS 02-JUN-2005  
 DEFINITION Pan troglodytes MTF1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION DQ052866

VERSION DQ052866.1 GI:66898813

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

## ORGANISM

Pan troglodytes  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Pan.

REFERENCE 1 (bases 1 to 1831)

## AUTHORS

Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,  
 Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civeello,D.,  
 White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

A Scan for Positively Selected Genes in the Genomes of Humans and

Chimpanzees

(er) PLOS Biol. 3 (6), E170 (2005)

JOURNAL PUBMED

REFERENCE 2 (bases 1 to 1831)

## AUTHORS

Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,  
 Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civeello,D.,  
 White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

## JOURNAL

Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.

## FEATURES

Location/Qualifiers

1..1831

/organism="Pan troglodytes"

/mol\_type="genomic DNA"

/db\_xref="taxon:9598"

<1..>1831

/gene="MTF1"

/locus\_tag="HCL13398"

## ORIGIN

Query Match 81.0%; Score 17; DB 11; Length 1831;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGGGG 21  
 |||||

DB 458 GTGCTGTAGTGGGGG 442  
 |||||

Search completed: January 27, 2006, 07:06:35  
 Job time : 1560.5 secs

This page blank (uspo<sup>te</sup>)



GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 27, 2006, 04:38:14 ; Search time 1554.5 Seconds  
(without alignments)  
632.055 Million cell updates/sec

Title: US-10-070-415A-1

Perfect score: 21

Sequence: 1 cccgtgaggaactwtgtct.21

Scoring table: IDENTITY NUC

Gapop 10.0 ; Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_est3:\*

4: gb\_hic:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_est7:\*

9: gb\_gss1:\*

10: gb\_gss2:\*

11: gb\_gss3:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	85.7	197	2	BB245383 BB245383
2	18	85.7	290	1	BB091924 BB091924
3	18	85.7	310	1	BB042602 BB042602
C 4	18	85.7	653	5	BW844757 BW844757
C 5	17.8	84.8	403	7	CO858932 LM SL5 00
6	17.8	84.8	747	5	BU427835 BU427835
7	17.6	83.8	785	10	CE322782 tigr-gss-
8	17.6	83.8	858	5	BU214119 603756067
9	17.4	82.9	266	2	BB566123 BB566123
10	17.4	82.9	378	5	BQ55287 BQ55287
C 11	17.4	82.9	520	9	AZ622420 AZ622420
C 12	17.4	82.9	536	9	AZ373738 LM0156F01
13	17.4	82.9	559	1	AL773761 AL773761
14	17.4	82.9	582	10	CW879538 CW879538
C 15	17.4	82.9	595	3	BJ100164 BJ100164
C 16	17.4	82.9	610	1	AL963378 AL963378
C 17	17.4	82.9	611	10	CE726956 CE726956
18	17.4	82.9	629	10	CZ408044 CZ408044
19	17.4	82.9	642	1	AL864604 AL864604
20	17.4	82.9	683	6	CA845679 CA845679
21	17.4	82.9	759	10	AG484074 AG484074
22	17.4	82.9	764	11	CR010258 Reverse s



Okazaki, Y. and Hayashizaki, Y.  
Automated filtration-based high-throughput plasmid preparation  
system. Genome Res. 9 (5), 463-470 (1999)  
Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,  
19-44 (1999)  
Please visit our web site (<http://genome.rtc.riken.go.jp>) for  
further details.

## FEATURES

Location/Qualifiers  
1..290  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="9430032C22"  
/tissue\_type="embryonic body between diaphragm region and  
neck"  
/dev\_stage="12 days embryo"  
/lab\_host="DH10B"  
/clone\_lib="RIKEN full-length enriched, 12 days embryo,  
embryonic body between diaphragm region and neck"  
/note="Site 1: SalI; Site 2: BamHI; cDNA library was  
prepared and sequenced in Mouse Genome Encyclopedia  
Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in  
RIKEN. Division of Experimental Animal Research in Riken  
contributed to prepare mouse tissues. 1st strand cDNA was  
primed with a primer [5'  
GAGAGAGAGAGGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was  
prepared by using trehalose thermo-activated reverse  
transcriptase and subsequently enriched for full-length by  
cap-trapper. cDNA went through one round of normalization  
to Rot = 20.0 and subtraction to Rot = 370.0. Second  
strand cDNA was prepared with the primer adapter of  
sequence [5' GAGAGAGATTCGAGTTAATTAATTAATTCCTCCCCCCCC  
3']. cDNA was cleaved with XhoI and BamHI."

## ORIGIN

Query Match 85.7%; Score 18; DB 1; Length 290;  
Best Local Similarity 90.0%; Pred. No. 5.5e+02;  
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAACCTGCTC 20

DB 219 CCCTGTGAGGAACCTGCTC 238

## RESULT 3

BB042602

LOCUS BB042602 RIKEN full-length enriched, 13 days embryo male testis Mus  
musculus cDNA clone 6030464H05 3', mRNA sequence.

BB042602

VERSION BB042602.1 GI:8448998

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T.,  
Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,  
Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,  
Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,  
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C.,  
Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H.,  
Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K.,  
Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T.,  
Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A.,  
Takahashi, F., Tomimaga, N., Toya, T., Tsunoda, Y., Watahiki, A.,  
Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A.,  
Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and  
Hayashizaki, Y.

TITLE  
JOURNAL  
COMMENT

RIKEN Mouse ESTs (Konno, H., et al.)  
Unpublished (2000)  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Sueniro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>  
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S.,  
Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Thermotabilization and thermotactivation of thermostable enzymes by  
trehalose and its application for the synthesis of full length  
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)  
Itoh, M., Kitaura, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,  
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,  
Okazaki, Y. and Hayashizaki, Y.  
Automated filtration-based high-throughput plasmid preparation  
system. Genome Res. 9 (5), 463-470 (1999)  
Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,  
19-44 (1999)  
Please visit our web site (<http://genome.rtc.riken.go.jp>) for  
further details.

## FEATURES

Location/Qualifiers  
1..310  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strains="CS7BL/6J"  
/db\_xref="taxon:10090"  
/clone="6030464H05"  
/sex="male"  
/tissue\_type="testis"  
/dev\_stage="13 days embryo"  
/lab\_host="DH10B"  
/clone\_lib="RIKEN full-length enriched, 13 days embryo  
male testis"  
/note="Site 1: SalI; Site 2: BamHI; cDNA library was  
prepared and sequenced in Mouse Genome Encyclopedia  
Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in  
RIKEN. Division of Experimental Animal Research in Riken  
contributed to prepare mouse tissues. 1st strand cDNA was  
primed with a primer [5'  
GAGAGAGAGGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was  
prepared by using trehalose thermo-activated reverse  
transcriptase and subsequently enriched for full-length by  
cap-trapper. cDNA went through one round of normalization  
to Rot = 5.0 and subtraction to Rot = 100.0. Second strand  
cDNA was prepared with the primer adapter of sequence [5'  
GAGAGAGATTCGAGTTAATTAATTAATTCCTCCCCCCC 3']. cDNA  
was cloned into the XhoI and BamHI sites. Vector: a  
modified pBluescript KS(+) after bulk excision from Lambda  
FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."

## ORIGIN

Query Match 85.7%; Score 18; DB 1; Length 310;  
Best Local Similarity 90.0%; Pred. No. 5.6e+02;  
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAACCTGCTC 20

DB 242 CCCTGTGAGGAACCTGCTC 261

## RESULT 4

BB044757/c

LOCUS BB044757

DEFINITION

5', mRNA sequence.

ACCESSION

BB044757

BB044757 653 bp mRNA linear EST 23-MAY-2005  
BB044757 Amphioxus Branchiostoma floridae unpublished cDNA library,  
neurula whole animal Branchiostoma floridae cDNA clone B0ne023019  
5', mRNA sequence.  
BB044757

```

VERSION      BW844757.1  GI:66452973
KEYWORDS     EST.
SOURCE       Branchiostoma floridae (Florida lancelet)
ORGANISM     Branchiostoma floridae
              Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
              Branchiostoma.
REFERENCE    1 (bases 1 to 653)
AUTHORS      Yu, J., Holland, L.Z., Shin-i, T., Kohara, Y., Satou, Y. and Satoh, N.
TITLE        Expressed genes in Branchiostoma floridae
JOURNAL      Unpublished (2005)
COMMENT      Contact: Tadasu Shin-i
              Center For Genetic Resource Information
              National Institute of Genetics
              1111 Yata, Mishima, Shizuoka 411-8540, Japan
              Tel: 81-559-81-6856
              Fax: 81-559-81-6855
              Email: tshini@genes.nig.ac.jp.
FEATURES     Location/Qualifiers
              1..653
                /organism="Branchiostoma floridae"
                /mol_type="mRNA"
                /db_xref="taxon:7739"
                /clone="bbs023o19"
                /tissue_type="whole animal"
                /dev_stage="neurula"
                /clone_lib="Amphioxus Branchiostoma floridae unpublished
                cDNA library, neurula whole animal"
ORIGIN
Query Match      85.7%; Score 18; DB 5; Length 653;
Best Local Similarity 90.0%; Pred. No. 6.4e+02;
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 CCTGTGAGGAACCTGCTCT 21
        |||||
Db      188 CCTGTGAGGACCTGCTCT 169

RESULT 5
CO858932/c
LOCUS      CO858932
DEFINITION LM SL5.004334 Locusta migratoria solitaria phase's hind-legs cDNA
            library Locusta migratoria cDNA, mRNA sequence.
ACCESSION  CO858932
VERSION     CO858932.1  GI:55918739
KEYWORDS   EST.
SOURCE     Locusta migratoria (migratory locust)
ORGANISM   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Orthopteroidea; Orthoptera; Acridomorpha;
            Acridoidea; Acrididae; Oedipodinae; Locusta.
REFERENCE  1 (bases 1 to 403)
AUTHORS    Kang, L., Chen, X., Zhou, Y., Liu, B., Zheng, W., Li, R., Wang, J. and
            Yu, J.
TITLE      The analysis of large-scale gene expression correlated to the phase
            changes of the migratory locust
JOURNAL    Proc. Natl. Acad. Sci. U.S.A. 101 (51), 17611-17615 (2004)
PUBMED    15591108
COMMENT    Contact: Le Kang
            National Laboratory of Integrated Management of Insect Pests and
            Rodents
            Institute of zoology, Chinese Academy of Sciences
            25 Beisihuanxi Road, Haidian, Beijing, 100080, China
            Tel: 86-10-68597439
            Fax: 86-10-68597486
            Email: lkang@panda.ios.ac.cn
            High quality sequence stop: 403.
FEATURES     Location/Qualifiers
              1..403
                /organism="Locusta migratoria"
                /mol_type="mRNA"
                /db_xref="taxon:7004"
                /tissue_type="hind-legs"

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/dev_stage="fifth-instar"
/clone_lib="Locusta migratoria solitaria phase's
hind-legs cDNA library"

ORIGIN
Query Match      84.8%; Score 17.8; DB 7; Length 403;
Best Local Similarity 90.5%; Pred. No. 7.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCTGTGAGGAACCTGCTCT 21
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Db      62 CCTGTGAGGACCTGCTCT 42

RESULT 6
BU427835
LOCUS      BU427835
DEFINITION BU427835.1  GI:25920511
            sequence.
ACCESSION  BU427835
VERSION     BU427835
KEYWORDS   EST.
SOURCE     Gallus gallus (chicken)
ORGANISM   Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
            1 (bases 1 to 747)
REFERENCE  Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
            Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
            A Comprehensive Collection of Chicken cDNAs
            Curr. Biol. 12 (22), 1965-1969 (2002)
            12445392
COMMENT    Contact: Simon Hubbard
            Department of Biomolecular Sciences
            University of Manchester Institute of Science and Technology
            (UMIST)
            PO Box 88, Manchester, M60 1QD, UK
            Tel: 01612008930
            Fax: 01612360409
            Email: Simon.Hubbard@umist.ac.uk.
            Location/Qualifiers
              1..747
                /organism="Gallus gallus"
                /mol_type="mRNA"
                /strain="Layer and broiler"
                /db_xref="taxon:9031"
                /clone="CHEST228b23"
                /sex="Male and female"
                /tissue_type="Chondrocytes isolated from growth plate
                cartilage"
                /dev_stage="adult"
                /lab_host="DH10B"
                /clone_lib="CSEQRBN09"
            /notes="Vector: pBluescript II KS(+); Site 1: EcoRI;
            Site 2: NotI; this normalized library was constructed from
            1 million independent clones. cDNA synthesis was initiated
            using an oligo(dT) primer, using methylated C in the first
            strand synthesis reaction. Following this first strand
            reaction, double-stranded cDNA was blunted, ligated and
            NotI adapters, digested with EcoRI, size-selected, and
            cloned into the NotI and EcoRI compatible sites of a
            custom modified MCS of the pBluescript (KS+) vector. The
            library was normalized in 2 rounds using conditions
            adapted from Soares et al., PNAS (1994) 91: 9228-9232 and
            Bonaldo et al., Genome Research 6 (1996): 791, except that
            a significantly longer reannealing hybridization was
            used."

ORIGIN
Query Match      84.8%; Score 17.8; DB 5; Length 747;
Best Local Similarity 90.5%; Pred. No. 8.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 CCTGTGAGGAAGTCTGTCT 21  
 DB 425 CCTGTGAGGAGCTGTCT 445

RESULT 7  
 CE322782 785 bp DNA linear GSS 26-SEP-2003  
 LOCUS tigr-gss-dog-17000361363031 Dog Library Canis familiaris genomic,  
 DEFINITION genomic survey sequence.  
 ACCESSION CE322782  
 VERSION CE322782.1 GI:361311132  
 KEYWORDS GSS:  
 SOURCE Canis familiaris (dog)  
 ORGANISM Canis familiaris  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
 Canis.  
 1 (bases 1 to 785)  
 REFERENCE Kirksness,E.F., Batna,V., Halpern,A.L., Levy,S., Remington,K.,  
 AUTHORS Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and  
 Venter,J.C.  
 TITLE The dog genome: survey sequencing and comparative analysis  
 JOURNAL Science 301 (5641), 1898-1903 (2003)  
 PUBMED 14512627  
 COMMENT Contact: Kirksness EF  
 The Institute for Genomic Research  
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
 Rockville, MD 20850, USA  
 Tel: 301-838-0200  
 Fax: 301-838-0208  
 Email: ekirksnes@tigr.org  
 Class: shotgun.

FEATURES  
 source Location/Qualifiers  
 1..785  
 /organism="Canis familiaris"  
 /mol\_type="genomic DNA"  
 /strain="Standard Poodle"  
 /db\_xref="taxon:9615"  
 /clone\_lib="Dog Library"  
 /note="Site 1: BstXI; Libraries were prepared from  
 peripheral blood"

ORIGIN  
 Query Match 83.8%; Score 17.6; DB 10; Length 785;  
 Best Local Similarity 94.4%; Pred. No. 1.1e+03;  
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 TGTGAGGAAGTCTGTCT 21  
 DB 501 TGTGAGGAAGTCTGTCT 518

RESULT 8  
 BU214119 858 bp mRNA linear EST 25-NOV-2002  
 LOCUS 603756067F1 CSEQCHN04 Gallus gallus cDNA clone ChEST667e17 5', mRNA  
 DEFINITION sequence.  
 ACCESSION BU214119  
 VERSION BU214119.1 GI:25389868  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 1 (bases 1 to 858)  
 REFERENCE Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,  
 AUTHORS Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.  
 TITLE A Comprehensive Collection of Chicken cDNAs  
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
 PUBMED 12445392

COMMENT Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology  
 (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.  
 Location/Qualifiers  
 1..858  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="White Leghorn, Hisex"  
 /db\_xref="taxon:9031"  
 /clone="ChEST667e17"  
 /tissue\_type="whole embryo"  
 /dev\_stage="20-21"  
 /lab\_host="DH10B"  
 /clone\_lib="CSEQCHN04"  
 /note="Organ: whole embryo; Vector: pBluescript II KS(+);  
 Site 1: EcoRI; Site 2: NotI; This normalized library was  
 constructed from 1 million independent clones. cDNA  
 synthesis was initiated using an oligo(dT) primer, using  
 methylated C in the first strand synthesis reaction.  
 Following this first strand reaction, double-stranded cDNA  
 was bluntended, ligated to NotI adapters, digested with  
 EcoRI, size-selected, and cloned into the NotI and EcoRI  
 compatible sites of a custom modified MCS of the  
 pBluescript (KS+) vector. The library was normalized in 2  
 rounds using conditions adapted from Soares et al., PNAS  
 (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6  
 (1996): 791, except that a significantly longer  
 reannealing hybridization was used."

ORIGIN  
 Query Match 83.8%; Score 17.6; DB 5; Length 858;  
 Best Local Similarity 94.4%; Pred. No. 1.1e+03;  
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 CTGTGAGGAAGTCTGTCT 20  
 DB 775 CTGTGAGGAAGTCTGTCT 792

RESULT 9  
 BB566123 266 bp mRNA linear EST 29-NOV-2000  
 LOCUS BB566123 RIKEN full-length enriched, 13 days embryo liver Mus  
 DEFINITION musculus cDNA clone 250002A19 5', mRNA sequence.  
 ACCESSION BB566123  
 VERSION BB566123.1 GI:11457015  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridea; Muridae; Murinae; Mus.  
 1 (bases 1 to 266)  
 REFERENCE Aizawa,K., Akahira,S., Akimura,T., Arai,A., Arakawa,T.,  
 AUTHORS Carninci,P., Hanagaki,T., Hayatsu,N., Hirooka,T., Hirozane,T.,  
 Hodoiyama,Y., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kawai,J.,  
 Kojima,Y., Konno,H., Kusakabe,M., Matsuyama,T., Miyazaki,A.,  
 Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y.,  
 Okido,T., Owa,C., Sakai,C., Sakai,K., Sasaki,D., Sato,K.,  
 Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,  
 Suzuki,H., Tagawa,A., Takahashi,F., Tanaka,T., Toya,T.,  
 Watahiki,A., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshiki,A.,  
 Yamamatsu,M. and Hayashizaki,Y.  
 RIKEN Mouse ESTs (Aizawa,K. et al. 2000)  
 Unpublished (2000)  
 Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic  
 Sciences Center (GSC), Yokohama Institute



Seq primer: CCGTGTAAACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 520.

## FEATURES

source

1..520  
 /Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0459C13"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 82.9%; Score 17.4; DB 9; Length 520;

Best Local Similarity 85.7%; Pred. No. 1.2e+03;

Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 CCCTGTGAGGAAGTCTGTCT 21

||||| ||||| ||||| |||||

Db 494 CCCTGTGAGGAAGTCTGTCT 474

## RESULT 12

AZ373738

LOCUS

DEFINITION AZ373738.1 GI:10487438 536 bp DNA linear GSS 02-OCT-2000  
 clone UUGC1M0126F01 F, Genomic survey sequence.

ACCESSION

AZ373738

VERSION

GSS.

KEYWORDS

Mus musculus

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Scuriognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 536)

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von

Niederhauser,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

## FEATURES

source

Plate: 0126 row: F column: 01  
 Seq primer: CCGTGTAAACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 536.

1..536  
 /Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0126F01"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 82.9%; Score 17.4; DB 9; Length 536;

Best Local Similarity 85.7%; Pred. No. 1.2e+03;

Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 CCCTGTGAGGAAGTCTGTCT 21

||||| ||||| ||||| |||||

Db 493 CCCTGTGAGGACTACCGTCT 513

## RESULT 13

AL773761

LOCUS

DEFINITION AL773761 XGC-gastrula Xenopus tropicalis cDNA clone Tgas071p03 5',  
 mRNA sequence.

ACCESSION

AL773761

VERSION

EST.

KEYWORDS

Xenopus tropicalis (western clawed frog)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;

Xenopodinae; Xenopus; Silurana.

REFERENCE

AUTHORS

1 (bases 1 to 559)

Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.

Sanger Xenopus tropicalis EST project 2001 (11\_2003)

Unpublished (2003)

On Jun 25, 2002 this sequence version replaced gi:21559465.

CONTACT: Taylor R

Sanger Institute

Hinxton, Cambridgeshire, CB10 1SA, UK

Email: tropesanger.ac.uk

This sequence is from a Xenopus Gene Collection (XGC) library

constructed by Aaron M. Zorn.

cDNA was oligo dT primed from 5ug of poly A+ RNA from stages 10-13

gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with

EcoRI at the 5' end and NotI at the 3' end.

Vector: pCS107; Site1: EcoRI; Site2: NotI

Host: Escherichia coli XL1-blue



Sanger Xenopus tropicalis EST project 2001  
TROPICALIS\_SEQUENCE\_ID: Tgas07ip03.picSp6  
Sequencing primer: SP6.

# FEATURES

Location/Qualifiers

1..559  
/organism="Xenopus tropicalis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8364"  
/clone="Tgas07ip03"  
/lab\_host="Escherichia coli XL1-blue"  
/dev\_stage="gastrula (stages 10.5-12 mixed)"  
/clone\_lib="XGC-gastrula"  
/note="Vector: pCS107; Site\_1: EcoRI; Site\_2: NotI; cDNA was oligo dt primed from sug of poly A+ RNA from stages 10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."

## ORIGIN

Query Match 82.9%; Score 17.4; DB 1; Length 559;  
Best Local Similarity 85.7%; Pred. No. 1.3e+03;  
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGCT 21

DB 246 CCATGTGAGGAAGTACTGACT 266

## RESULT 14

### CW879538

#### LOCUS

DEFINITION CW879538 582 bp DNA linear GSS 12-FEB-2005  
shS2kd38-90.b\_094.ab1 Whole-genome shotgun library of the elephant  
shark (aka elephant fish) Callorhynchus milii genomic, genomic  
survey sequence.

#### ACCESSION

#### VERSION

#### KEYWORDS

#### SOURCE

#### ORGANISM

#### REFERENCE

#### AUTHORS

#### TITLE

#### JOURNAL

#### PUBMED

#### COMMENT

Callorhynchus milii (elephantfish)  
Callorhynchus milii  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
Holocephali; Chimaeriformes; Callorhynchidae; Callorhynchus.  
1 (bases 1 to 582)  
Venkatesh, B., Ray, A., Dandona, N., Patil, J. G. and Brenner, S.  
A compact cartilaginous fish model genome  
Curr. Biol. 15 (3), R82-R83 (2005)  
15694293  
Contact: Venkatesh B  
Molecular Genetics Lab  
Institute of Molecular and Cell Biology  
61 Biopolis Drive, Singapore 138673  
Tel: 65 6586 9571  
Fax: 65 6779 1117  
Email: mcbv@imcb.a-star.edu.sg  
Whole-genome shotgun sequences of the elephant shark (aka elephant  
fish)  
Class: shotgun.

## FEATURES

### source

Location/Qualifiers

1..582  
/organism="Callorhynchus milii"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7868"  
/sex="Male"  
/tissue\_type="Testis"  
/clone\_lib="Whole-genome shotgun library of the elephant  
shark (aka elephant fish)"

## ORIGIN

Query Match 82.9%; Score 17.4; DB 10; Length 582;  
Best Local Similarity 85.7%; Pred. No. 1.3e+03;  
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGCT 21

|||||

DB 141 CTCGTGAGGAATTTCTGTCT 161

## RESULT 15

### BJ100164/c

#### LOCUS

#### DEFINITION

#### ACCESSION

#### VERSION

#### KEYWORDS

#### SOURCE

#### ORGANISM

#### REFERENCE

#### AUTHORS

#### TITLE

#### JOURNAL

#### COMMENT

#### FEATURES

#### source

#### Location/Qualifiers

#### Expressed genes in X. laevis embryo

#### Unpublished (2001)

#### Contact: Tadasu Shin-i

#### Center For Genetic Resource Information

#### National Institute of Genetics

#### 1111 Yata, Mishima, Shizuoka 411-8540, Japan

#### Tel: 81-559-81-6856

#### Fax: 81-559-81-6855

#### Email: tshini@genes.nig.ac.jp

#### The information of this clone is available through the following

#### URL.

#### http://xenopus.nibb.ac.jp.

#### Location/Qualifiers

#### 1..595

#### /organism="Xenopus laevis"

#### /mol\_type="mRNA"

#### /db\_xref="taxon:8355"

#### /clone="XL173k02"

#### /tissue\_type="whole embryo"

#### /dev\_stage="stage 10.5"

#### /clone\_lib="NIBB Mochii normalized Xenopus early gastrula

#### library"

#### ORIGIN

#### Query Match

#### Best Local Similarity

#### Matches

#### 18; Conservative

#### 1; Mismatches

#### 2; Indels

#### 0; Gaps

#### 0;

#### QY

#### 1 CCTGTGAGGAAGTCTGCT 21

#### DB

#### 214 CCATGTGAGGAAGTACTGCT 194

#### RESULT 16

### AL963378

#### LOCUS

#### DEFINITION

#### ACCESSION

#### VERSION

#### KEYWORDS

#### SOURCE

#### ORGANISM

#### REFERENCE

#### AUTHORS

#### TITLE

#### JOURNAL

#### COMMENT

#### Query Match

#### Best Local Similarity

#### Matches

#### 18; Conservative

#### 1; Mismatches

#### 2; Indels

#### 0; Gaps

#### 0;

#### QY

#### 1 CCTGTGAGGAAGTCTGCT 21

#### |||||

BJ100164 595 bp mRNA linear EST 01-OCT-2003  
BJ100164 NIBB Mochii normalized Xenopus early gastrula library  
Xenopus laevis cDNA clone XL173k02 3', mRNA sequence.

EST.

BJ100164.1 GI:17602807

Xenopus laevis (African clawed frog)

Xenopus laevis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

Xenopodinae; Xenopus; Xenopus.

1 (bases 1 to 595)

Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and

Kohara, Y.

Expressed genes in X. laevis embryo

Unpublished (2001)

Contact: Tadasu Shin-i

Center For Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tshini@genes.nig.ac.jp

The information of this clone is available through the following

URL.

http://xenopus.nibb.ac.jp.

Location/Qualifiers

1..595

/organism="Xenopus laevis"

/mol\_type="mRNA"

/db\_xref="taxon:8355"

/clone="XL173k02"

/tissue\_type="whole embryo"

/dev\_stage="stage 10.5"

/clone\_lib="NIBB Mochii normalized Xenopus early gastrula

library"

Query Match 82.9%; Score 17.4; DB 3; Length 595;

Best Local Similarity 85.7%; Pred. No. 1.3e+03;

Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

0;

QY

1 CCTGTGAGGAAGTCTGCT 21

DB

214 CCATGTGAGGAAGTACTGCT 194

AL963378 610 bp mRNA linear EST 05-DEC-2003

AL963378 XGC-gastrula Xenopus tropicalis cDNA clone Tgas133g15 5',

mRNA sequence.

AL963378.2 GI:139014143

Xenopus tropicalis (western clawed frog)

Xenopus tropicalis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

Xenopodinae; Xenopus; Silurana.

1 (bases 1 to 610)

Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J.

Sanger Xenopus tropicalis EST project 2001 (11\_2003)

Unpublished (2003)

On Nov 27, 2002 this sequence version replaced gi:25786973.

Contact: Taylor R

Sanger Institute

Hinxton, Cambridgeshire, CB10 1SA, UK



Email: trop@sanger.ac.uk  
 Sanger Xenopus tropicalis EST project 2001  
 TROPICALIS SEQUENCE ID: TGa133g15.plkSP6  
 Sequencing primer: SP6  
 This sequence is from a Xenopus Gene Collection (XGC) library  
 constructed by Aaron M. Zorn.  
 cDNA was oligo dt primed from 5ug of poly A+ RNA from stages 10-13  
 gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with  
 EcoRI at the 5' end and NotI at the 3' end.  
 Vector: pCS107; Site 1: EcoRI; Site 2: NotI  
 Host: Escherichia coli XL1-blue.

## FEATURES

source

1. .610  
 /organism="Xenopus tropicalis"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:8364"  
 /clone="TGa133g15"  
 /dev\_stage="gastrula (stages 10.5-12 mixed)"  
 /lab\_host="Escherichia coli XL1-blue"  
 /clone\_lib="XGC-gastrula"  
 /notes="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA  
 was oligo dt primed from 5ug of poly A+ RNA from stages  
 10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated  
 into pCS107 with EcoRI at the 5' end and NotI at the 3'  
 end."

## ORIGIN

Query Match 82.9%; Score 17.4; DB 1; Length 610;  
 Best Local Similarity 85.7%; Pred. No. 1.3e+03;  
 Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21  
 |||||||||  
 Db 161 CCATGTGAGGAAGTCTGACT 181

## RESULT 17

CE726956/c

LOCUS

DEFINITION 611 bp DNA linear GSS 30-SEP-2003  
 tigr-g88-dog-17000315262749 Dog Library Canis familiaris genomic,  
 genomic survey sequence.

CE726956

GSS.

CE726956.1 GI:37067076

SOURCE

Canis familiaris (dog)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
 Canis.

## REFERENCE

AUTHORS

1 (bases 1 to 611)  
 Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,  
 Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and  
 Venter, J.C.

The dog genome: survey sequencing and comparative analysis

PUBMED

14512627

Contact: Kirkness EF

The Institute for Genomic Research

Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,

Rockville, MD 20850, USA

Tel: 301-838-0200

Fax: 301-838-0208

Email: ekirknes@tigr.org

Class: shotgun.

Location/Qualifiers

1. .611

/organism="Canis familiaris"

/mol\_type="genomic DNA"

/strain="Standard Poodle"

/db\_xref="taxon:9615"

/clone\_lib="Dog Library"

/note="Site 1: BstXI; Libraries were prepared from

peripheral blood"

## ORIGIN

Query Match 82.9%; Score 17.4; DB 10; Length 611;  
 Best Local Similarity 85.7%; Pred. No. 1.3e+03;  
 Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21

Db 173 CCTGTGAGGAAGTCTGTCT 153

## RESULT 18

CZ408044

LOCUS

DEFINITION 629 bp DNA linear GSS 06-APR-2005  
 1003747 RP42 Bos taurus genomic clone RP42-14N03, genomic survey  
 sequence.

ACCESSION

CZ408044

VERSION

CZ408044.1

KEYWORDS

GSS.

SOURCE

Bos taurus (cow)

ORGANISM

Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;

Pecora; Bovidae; Bovinae; Bos.

1 (bases 1 to 629)

Sonstegard, T.S., Van Tassel, C.P., Capuco, A.V., de Jong, P.,

Matukumalli, L.K., Shade, L.S., Bosak, S., Rubenfield, M. and

Gaebler, L.C.

Bovine BAC End Sequences from Library RPCI-42

Unpublished (2005)

Contact: Tad S. Sonstegard

Bovine Functional Genomics Laboratory

Animal and Natural Resources Institute

Bldg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA

Tel: 3015048416

Fax: 3015048414

Email: tads@anri.barc.usda.gov

Clones are derived from the bovine BAC library RPCI-42

(http://bacpac.chori.org/mbovine42.htm). For BAC library

availability, please contact Pieter de Jong (pdejong@mail.choi.org).

Clones may be purchased from BACPAC Resources

(http://www.chori.org/bacpac/ordering\_information.htm). This work

was undertaken as part of the International Bovine BAC Mapping

Consortium (IBBMC) by USDA-ARS-BFGL.

Plate: 14 row: N column: 03

Seq primer: CTGGCCGTCGACATTAGG

Class: BAC ends.

Location/Qualifiers

1. .629

/organism="Bos taurus"

/mol\_type="genomic DNA"

/strain="Holstein"

/db\_xref="taxon:9913"

/clone="RP42-14N03"

/sex="male"

/cell\_type="Blood"

/clone\_lib="RP42"

/note="Vector: pBACe3.6; Site 1: MboI; Site 2: MboI;

RPCI-42 Bovine BAC library (Male Holstein) produced by

Pieter de Jong"

Query Match 82.9%; Score 17.4; DB 10; Length 629;

Best Local Similarity 85.7%; Pred. No. 1.3e+03;

Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21

Db 462 CACTGTGAGGTACTACTGTCT 482

## RESULT 19

AL864604

```

LOCUS       AL864604                642 bp    mRNA    linear    EST 03-DEC-2003
DEFINITION   AL864604 XGC-egg Xenopus tropicalis cDNA clone fEgg131a01 5', mRNA
sequence.
ACCESSION    AL864604
VERSION      AL864604.2   GI:38659306
KEYWORDS     EST.
SOURCE       Xenopus tropicalis (western clawed frog)
ORGANISM     Xenopus tropicalis
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
              Xenopodinae; Xenopus; Silurana.
REFERENCE    1 (bases 1 to 642)
              Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
              Sanger Xenopus tropicalis EST project 2001 (11_2003)
              Unpublished (2003)
              On Sep 15, 2002 this sequence version replaced gi:22884869.
COMMENT      Contact: Taylor R
              Sanger Institute
              Hinxton, Cambridgeshire, CB10 1SA, UK
              Email: trop@sanger.ac.uk
              Sanger Xenopus tropicalis EST project 2001
              TROPICALIS SEQUENCE ID: TEGg131a01.plkSP6
              Sequencing primer: SP6
              This sequence is from a Xenopus Gene Collection (XGC) library
              constructed by Aaron M. Zorn.
              cDNA was oligo dt primed from 5ug of poly A+ RNA from egg.
              EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
              5' end and NotI at the 3' end.
              Vector: pCS107; Site 1: EcoRI; Site 2: NotI
              Host: Escherichia coli XL1-blue.
              Location/Qualifiers
                1..642
                 /organism="Xenopus tropicalis"
                 /mol_type="mRNA"
                 /db_xref="taxon:8364"
                 /clone="TEGg131a01"
                 /dev_stage="egg"
                 /lab_host="Escherichia coli XL1-blue"
                 /clone_lib="XGC-egg"
                 /note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
                 was oligo dt primed from 5ug of poly A+ RNA from egg.
                 EcoRI-NotI cut cDNA was then ligated into pCS107 with
                 EcoRI at the 5' end and NotI at the 3' end"

ORIGIN
Query Match      82.9%;   Score 17.4;   DB 1;   Length 642;
Best Local Similarity 85.7%;   Pred. No. 1.3e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1  CCTGTGAGGAACCTGCTGTCT 21
        |||||||
Db      225 CCATGTGAGGAACCTGACT 245

RESULT 20
CAB45679
LOCUS       CAB45679                683 bp    mRNA    linear    EST 13-DEC-2002
DEFINITION   hab72h11.y2 Fugu hgmPB adult spleen Takifugu rubripes cDNA clone
IMAGE:6354285 5', mRNA sequence.
ACCESSION    CAB45679
VERSION      CAB45679.1   GI:26775056
KEYWORDS     EST.
SOURCE       Takifugu rubripes (Fugu rubripes)
ORGANISM     Takifugu rubripes
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
              Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
              Tetraodontidae; Tetraodontidae; Takifugu.
              1 (bases 1 to 683)
              Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
              Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
              Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
              Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,

```

```

Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
WashU Zebrafish EST Project 1998
Unpublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrfish@watson.wustl.edu
Library materials and construction by Greg Elgar (UK MRC HGMP-RC).
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Fugu clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: T3 ET from Amersham
High quality sequence stop: 496.
Location/Qualifiers
  1..683
   /organism="Takifugu rubripes"
   /mol_type="mRNA"
   /db_xref="taxon:31033"
   /clone="IMAGE:6354285"
   /dev_stage="adult"
   /lab_host="DH10B (T1-resistant)"
   /clone_lib="Fugu hgmPB adult spleen"
   /note="Organ: spleen; Vector: pBluescript II KS
   oligo-dT primed and directionally cloned using cDNA
   prepared with the Stratagene cDNA synthesis kit. Tissue
   source: adult spleen. Library materials and construction
   by Greg Elgar (UK MRC HGMP-RC)."

ORIGIN
Query Match      82.9%;   Score 17.4;   DB 6;   Length 683;
Best Local Similarity 85.7%;   Pred. No. 1.3e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1  CCTGTGAGGAACCTGCTGTCT 21
        |||||||
Db      330 CCCTGTGAGTACTGCTGTCT 350

RESULT 21
AG484074
LOCUS       AG484074                759 bp    DNA    linear    GSS 22-DEC-2004
DEFINITION   Mus musculus molossinus DNA, clone:MSMg01-379H12.T7, genomic survey
sequence.
ACCESSION    AG484074
VERSION      AG484074.1   GI:48191304
KEYWORDS     GSS.
SOURCE       Mus musculus molossinus (Japanese wild mouse)
ORGANISM     Mus musculus molossinus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
              Sciurognathi; Muridae; Murinae; Mus.
              1
              Abe,X., Noguchi,H., Tagawa,K., Yuzuriha,M., Toyoda,A., Kojima,T.,
              Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriwaki,K. and
              Shiroishi,T.
              Contribution of Asian mouse subspecies Mus musculus molossinus to
              genomic constitution of strain C57BL/6J, as defined by BAC-end
              sequence-SNP analysis
              Genome Res. 14 (12), 2439-2447 (2004)
              15574823
              2 (bases 1 to 759)
              Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
              Direct Submission
              Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
              and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
              1-7-22 Suehiro-chou,Tsukumi-ku, Yokohama, Kanagawa, 230-0045, Japan
              (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
              Tel:81-45-503-9111, Fax:81-45-503-9170)

```

```

COMMENT
Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : T7
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.

FEATURES
source
Location/Qualifiers
1..759
/mol_type="Mus musculus molossinus"
/sub_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-379H12.T7"
/sex="male"
/tissue type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"

ORIGIN
Query Match 82.9%; Score 17.4; DB 10; Length 759;
Best Local Similarity 85.7%; Pred. No. 1.3e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
||||| ||| ||||| |||||
DB 520 CCTGAGAGCAACTTCTGTCT 540

RESULT 22
LOCUS
DEFINITION
Reverse strand read from insert in 3'HPRT insertion targeting and
chromosome engineering clone MHP360C24, genomic survey sequence.
ACCESSION
CR010258
VERSION
1 GI:49743249
KEYWORDS
GSS; genome survey sequence; MICER.
SOURCE
Mus musculus
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 764)
AUTHORS
Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
Jongers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
Rogers,J. and Bradley,A.
DIRECT SUBMISSION
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. http://www.sanger.ac.uk/MICER

FEATURES
source
Location/Qualifiers
1..764
/mol_type="Mus musculus"
/sub_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHP360C24"
/clone_lib="MHP36"

ORIGIN
Query Match 82.9%; Score 17.4; DB 11; Length 764;
Best Local Similarity 85.7%; Pred. No. 1.3e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
||||| ||| ||||| |||||
DB 663 CCTGAGAGCAACTTCTGTCT 683

RESULT 23
LOCUS
DEFINITION
Reverse strand read from insert in 3'HPRT insertion targeting and
chromosome engineering clone MHP129123, genomic survey sequence.
ACCESSION
CR038774
VERSION
1 GI:49771829
KEYWORDS
GSS; genome survey sequence; MICER.
SOURCE
Mus musculus
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 784)
AUTHORS
Abe,K., Noguchi,H., Tagawa,K., Yuzuriha,M., Toyoda,A., Kojima,T.,
Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriwaki,K. and
Shiroishi,T.
DIRECT SUBMISSION
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : TJ
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.

FEATURES
source
Location/Qualifiers
1..784
/mol_type="Mus musculus molossinus"
/sub_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-460E18.TJ"
/sex="male"
/tissue type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"

ORIGIN
Query Match 82.9%; Score 17.4; DB 10; Length 784;
Best Local Similarity 85.7%; Pred. No. 1.3e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
||||| ||| ||||| |||||
DB 403 CCTGAGAGCAACTTCTGTCT 383

RESULT 24
LOCUS
DEFINITION
Reverse strand read from insert in 3'HPRT insertion targeting and
chromosome engineering clone MHP129123, genomic survey sequence.
ACCESSION
CR038774
VERSION
1 GI:49771829
KEYWORDS
GSS; genome survey sequence; MICER.
SOURCE
Mus musculus
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 825)  
Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L., Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y., Rogers,J. and Bradley,A.

## TITLE

Direct Submission  
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. <http://www.sanger.ac.uk/MICER>

## FEATURES

Location/Qualifiers

source

1..825  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
/clone="MHPPI29123"  
/clone\_lib="MHP"

## ORIGIN

Query Match 82.9%; Score 17.4; DB 11; Length 825;  
Best Local Similarity 85.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCTGTGAGCAACTTCTGTCT 21

Db 661 CCCTGAGCAACTTCTGTCT 681

## RESULT 25

DN033350

LOCUS

DN033350 DN033350.1 GI:59227941  
JGI\_CAAR9837.fwd NIH\_XGC\_tropliv1 Xenopus tropicalis cDNA clone  
IMAGE:7741910 5', mRNA sequence.

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 828)  
Richardson,P., Lucas,S., Rokhsar,D., Dettter,J.C., Ng,D.C., Brokstein,P. and Lindquist,E.A.  
DOE Joint Genome Institute Xenopus tropicalis EST project  
Unpublished (2004)  
Other ESTs: JGI CAAR9837.rev  
Contact: Lindquist,E.A., Richardson,P.  
DOE Joint Genome Institute  
2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
Tel: 925 296 5600  
Fax: 925 296 5710  
Email: cdna@jgi-psf.org  
Tissue Procurement: Robert M. Grainger  
cDNA Library Preparation: Bruce Blumberg Laboratory, University of California, Irvine  
DNA Sequencing: DOE Joint Genome Institute: <http://www.jgi.doe.gov>  
Clone Distribution: I.M.A.G.E. Consortium/LLNL:  
<http://image.llnl.gov>  
Naming Conventions: EST name is generated by the concatenation of the JGI Clone Id and the direction of sequencing. The suffix '.fwd' indicates a forward sequencing read of the insert. It does not necessarily reflect the orientation of the insert.  
Plate: CAAR 0101 row: i column: 12  
High quality sequence stop: 785.  
Location/Qualifiers

## FEATURES

source

1..828  
/organism="Xenopus tropicalis"  
/mol\_type="mRNA"  
/strain="N6 (Nigerian 6th generation inbred)"  
/db\_xref="taxon:8364"  
/clone="IMAGE:7741910"  
/sex="male"

/tissue\_type="Liver"

/dev\_stage="Adult"

/lab\_host="ElectroMAX DH10B T1 Phage resistant cells"  
/clone\_lib="NIH\_XGC\_tropliv1"

/note="Vector: PCS107; Site\_1: EcoRI; Site\_2: XhoI; The library was prepared from 5 ug of poly A+ RNA by oligo-dT priming  
(5'-GAGAGAGAGAGAGAGACTAGTCTCGAGTTTTTTTTTTTTTTT-3')

and Stratascript reverse transcriptase. After ligation of EcoRI adapters (5'-AATTCGACGAGG-3') followed by kinasing adapters and by XhoI digestion, the cDNA was size selected by chromatography on Sepharose CL-2B columns and fractions containing cDNAs larger than 1000 bp were ligated into EcoRI/XhoI-digested PCS107. Reference for library construction: Current Genomics 4, 635-644. Library constructed by Michelle Tabb and Bruce Blumberg (Dept of Developmental and Cell Biology, University of California, Irvine)."

## ORIGIN

Query Match 82.9%; Score 17.4; DB 8; Length 828;  
Best Local Similarity 85.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCTGTGAGCAACTTCTGTCT 21

Db 307 CCATGTGAGCAACTTCTGACT 327

## RESULT 26

DN074071/c

LOCUS

DN074071 DN074071.1 GI:596663039  
JGI\_CABD8095.rev NIH\_XGC\_troplun1 Xenopus tropicalis cDNA clone  
IMAGE:7813425 3', mRNA sequence.

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 854)  
Richardson,P., Lucas,S., Rokhsar,D., Dettter,J.C., Ng,D.C., Brokstein,P. and Lindquist,E.A.  
DOE Joint Genome Institute Xenopus tropicalis EST project  
Unpublished (2004)  
Other ESTs: JGI CABD8095.fwd  
Contact: Lindquist,E.A., Richardson,P.  
DOE Joint Genome Institute  
2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
Tel: 925 296 5600  
Fax: 925 296 5710  
Email: cdna@jgi-psf.org  
Tissue Procurement: Robert M. Grainger  
cDNA Library Preparation: Bruce Blumberg Laboratory, University of California, Irvine  
DNA Sequencing: DOE Joint Genome Institute: <http://www.jgi.doe.gov>  
Clone Distribution: I.M.A.G.E. Consortium/LLNL:  
<http://image.llnl.gov>  
Naming Conventions: EST name is generated by the concatenation of the JGI Clone Id and the direction of sequencing. The suffix '.rev' indicates a reverse sequencing read of the insert. It does not necessarily reflect the orientation of the insert.  
Plate: CABD 0085 row: m column: 7  
High quality sequence stop: 805.  
Location/Qualifiers

## FEATURES

source

1..854  
/organism="Xenopus tropicalis"  
/mol\_type="mRNA"  
/strain="N6 (Nigerian 6th generation inbred)"  
/db\_xref="taxon:8364"  
/clone="IMAGE:7813425"

```

/tissue_type="Lung"
/dev_stage="Adult"
/lab_host="ElectroMAX DH10B T1 Phage Resistant cells"
/clone_lib="NIH XGC tropLun1"
/notes="Vector: pCS107; Site_1: EcoRI; Site_2: XhoI; The library was prepared from 5 ug of poly A+ RNA by oligo-dT priming (5'-ACTAGTGGCGCGCTAGCCTCGAGTTTTTTTTTTTTTTT-3') and Stratascript reverse transcriptase. After ligation of EcoRI adaptors (5'-AATTCGGCAGGAG-3') followed by kinasing adaptors and by XhoI digestion, the cDNA was size selected by chromatography on Sepharose CL-2B columns and fractions containing cDNAs larger than 1000 bp were ligated into EcoRI/XhoI-digested pCS107. Reference for library construction: Current Genomics 4, 635-644. Library constructed by Michelle Tabb and Bruce Blumberg (Dept of Developmental and Cell Biology, University of California, Irvine)."

```

## ORIGIN

```

Query Match      82.9%; Score 17.4; DB 8; Length 854;
Best Local Similarity 85.7%; Pred. No. 1.4e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 CCTGTGAGGAAGTCTGTCT 21
   |||||
DB 429 CCATGTGAGGAAGTCTGACT 409

```

## RESULT 27

```

CX382809
LOCUS          880 bp mRNA linear EST 05-JAN-2005
DEFINITION    JGI XZT54022.fwd NIH XGC tropTad5 Xenopus tropicalis cDNA clone
IMAGE:7628684 5', mRNA sequence.

```

```

ACCESSION     CX382809
VERSION       CX382809.1 GI:57151366
KEYWORDS
SOURCE        Xenopus tropicalis (western clawed frog)

```

## ORGANISM

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.

```

## REFERENCE

```

AUTHORS       Richardson,P., Lucas,S., Rokhsar,D., Detter,J.C., Ng,D.C.,
               Brokstein,P. and Lindquist,E.A.

```

```

TITLE         DOE Joint Genome Institute Xenopus tropicalis EST project

```

```

JOURNAL       Unpublished (2004)

```

```

COMMENT       Contact: Lindquist,E.A., Richardson,P.
               DOE Joint Genome Institute
               2800 Mitchell Drive, Walnut Creek, CA 94598, USA
               Tel: 925 296 5600
               Fax: 925 296 5710
               Email: cdna@jgi-psf.org
               Tissue Procurement: Richard M. Harland Laboratory, University of
               California, Berkeley: http://tropicalis.berkeley.edu/home
               cDNA Library Preparation: Richard M. Harland Laboratory, University
               of California, Berkeley
               DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
               Clone Distribution: I.M.A.G.E. Consortium/LNL:
               http://image.lnl.gov

```

```

Naming Conventions: EST name is generated by the concatenation of
the JGI Clone Id and the direction of sequencing. The suffix '.fwd'
indicates a forward sequencing read of the insert. It does not
necessarily reflect the orientation of the insert.
Plate: XZT 0561 row: k column: 18
High quality sequence stop: 762.
Location/Qualifiers

```

## FEATURES

```

source

```

```

1..880
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="IMAGE:7628684"
/tissue_type="whole embryo"

```

```

/dev_stage="Tadpole (st. 36-41)"
/lab_host="E. coli XL1-Blue derivative, Stratagene
ElectroFen-Blue"
/clone_lib="NIH XGC tropTad5"
/notes="Vector: pCS107; Site_1: SalI; Site_2: NotI; Tadpole
library constructed by Russell B. Fletcher in R. Harland's
lab using poly A RNA and oligo dT primers (Invitrogen
SuperScript Plasmid System for cDNA Synthesis and
Cloning). SalI (5' end) -NotI (3' end) cDNA was inserted
into vector pCS107
(http://mcb.berkeley.edu/labs/harland/pages/plasmids.html)
"

```

## ORIGIN

```

Query Match      82.9%; Score 17.4; DB 8; Length 880;
Best Local Similarity 85.7%; Pred. No. 1.4e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 CCTGTGAGGAAGTCTGTCT 21
   |||||
DB 37 CCATGTGAGGAAGTCTGACT 57

```

## RESULT 28

```

BX751267
LOCUS          886 bp mRNA linear EST 09-DEC-2003
DEFINITION    BX751267 XGC-gastrula Xenopus tropicalis cDNA clone TGas071p03 3',
mRNA sequence.

```

```

ACCESSION     BX751267
VERSION       BX751267.1 GI:39641335
KEYWORDS
SOURCE        Xenopus tropicalis (western clawed frog)

```

## ORGANISM

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.

```

## REFERENCE

```

AUTHORS       Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
               Sanger Xenopus tropicalis EST project 2001 (11_2003)

```

```

TITLE         Unpublished (2003)

```

```

JOURNAL       Contact: Croning MDR

```

```

COMMENT       Sanger Institute
               Hinxtion, Cambridgeshire, CB10 1SA, UK

```

```

               Email: trop@sanger.ac.uk

```

```

               Sanger Xenopus tropicalis EST project 2001

```

```

               TROPICALIS_SEQUENCE_ID: TGas071p03.q1kT7

```

```

               Sequencing primer: T7

```

```

               This sequence is from a Xenopus Gene Collection (XGC) library
               constructed by Aaron M. Zorn.

```

```

               cDNA was oligo dT primed from 5ug of poly A+ RNA from stages 10-13
               gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with
               EcoRI at the 5' end and NotI at the 3' end.

```

```

               Vector: pCS107; Site_1: EcoRI; Site_2: NotI

```

```

               Host: Escherichia coli XL1-blue.

```

## FEATURES

```

source

```

```

1..886
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="TGas071p03"
/dev_stage="gastrula (stages 10.5-12 mixed)"
/lab_host="Escherichia coli XL1-blue"
/clone_lib="XGC-gastrula"
/notes="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
into pCS107 with EcoRI at the 5' end and NotI at the 3'
end."

```

## ORIGIN

```

Query Match      82.9%; Score 17.4; DB 5; Length 886;
Best Local Similarity 85.7%; Pred. No. 1.4e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

source

```
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ZMMBc0267B13"
/lab_host="E. coli DH10B"
/clone_lib="ZMMBc (EcoRI)"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"

ORIGIN
Query Match      82.9%; Score 17.4; DB 10; Length 1022;
Best Local Similarity 85.7%; Pred. No. 1.4e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
   |||||||:|||||
Db 868 CCGTGTGAGGAAGTCTGTCT 888

RESULT 32
CF223086
LOCUS
DEFINITION
AGENCOURT 15068014 NICHD XGC Emb7 Xenopus tropicalis cDNA clone
CF223086
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Xenopus; Silurana.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Robert M. Grainger
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LIAWI4629 row: n column: 04
High quality sequence start: 176
High quality sequence stop: 562.

FEATURES
source
1..1177
Location/Qualifiers
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="IMAGE:5976517"
/tissue_type="tailbud"
/dev_stage="embryo, stages 20-27"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NICHD XGC Emb7"
/note="Vector: pCMV-SPORT6.1; Site 1: NotI; Site 2: EcoRV;
Cloned unidirectionally. Primer: Oligo dT. Average insert
size 2.1 kb. Constructed by Invitrogen. Note: This is a
Xenopus Gene Collection (XGC) library."

ORIGIN
Query Match      82.9%; Score 17.4; DB 6; Length 1177;
Best Local Similarity 85.7%; Pred. No. 1.4e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
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Db 305 CCATGTGAGGAAGTCTGTCT 325

RESULT 33
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DEFINITION
DCBCKC03 DCB Homo sapiens cDNA, mRNA sequence.
BUI199108
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
Xu, X., Gu, J., Liu, F., Ou, J., Zhao, M., Li, Y., Huang, Q., Zhou, J.,
Song, H., Gu, Y., Yang, Y., Gao, G., Xiao, H., Li, N., Qian, B., Gao, X.,
Cheng, Z., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M.,
Lu, G., Cheng, Z. and Han, Z.
Homo sapiens cDNA DCB clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@hgsc.sh.cn.
Location/Qualifiers
1..2319
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/mol_type="mRNA"
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/cell_type="dendritic cells"
/dev_stage="mature"
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/clone_lib="DCB"
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Query Match      82.9%; Score 17.4; DB 5; Length 2319;
Best Local Similarity 85.7%; Pred. No. 1.6e+03;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21
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DEFINITION
BB466847 RIKEN full-length enriched, 12 days embryo eyeball Mus
musculus cDNA clone D23001A04 3', mRNA sequence.
BB466847
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Mus.
1 (bases 1 to 197)
Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T.,
Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C.,
Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H.,
Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K.,
Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Sugahara, Y., Suzuki, H., Tagawa, A.,
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Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.  
RIKEN Mouse ESTs (Konno, H., et al.)  
Unpublished (2000)  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome.res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/  
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)  
Itoh, M., Kitsuina, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.  
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)  
Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)  
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

## FEATURES

source

Location/Qualifiers

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/dev_stage="12 days embryo"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 12 days embryo
eyeball"
/note="Site 1: SalI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGAGAGAGCGCGCCCACTCGAGTTTCTTTTCTTTT 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5',
GAGAGAGAGTTCTCGAGTTAATTAATTAATCCCCCCCCCCC 3']. cDNA
was cleaved with BamHI and XhoI. Vector: a modified
pBluescript KS(+) after bulk excision from Lambda FLC I."
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## ORIGIN

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Query Match      81.0%; Score 17; DB 2; Length 197;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY  1  CCCTGTGAGGAACCTGCTGT 19
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Db   126 CCCTGTGAGGAACCTGCT 144
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RESULT 35
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LOCUS      BB287229 RIKEN full-length enriched, 2 cells egg Mus musculus cDNA
DEFINITION clone B020017L13 3', mRNA sequence.
ACCESSION BB287229
VERSION    BB287229.1 GI:8987678
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## KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS

1 (bases 1 to 262)

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Isnikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.  
RIKEN Mouse ESTs (Konno, H., et al.)  
Unpublished (2000)  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome.res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/  
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)  
Itoh, M., Kitsuina, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.  
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)  
Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)  
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

## TITLE

JOURNAL

COMMENT





COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/ Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Thermotabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh, M., Kiteunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999) Please visit our web site (http://genome.rtc.riken.go.jp) for further details.	
	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/ Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Thermotabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh, M., Kiteunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999) Please visit our web site (http://genome.rtc.riken.go.jp) for further details.	
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ORIGIN	Query Match 81.0%; Score 17; DB 2; Length 319; Best Local Similarity 89.5%; Pred. No. 1.8e+03; Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
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	LOCUS BB459406 RIKEN full-length enriched, 12 days embryo spinal ganglion DEFINITION Mus musculus cDNA clone D130061E08 3', mRNA sequence.	
VERSION	BB459406	
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KEYWORDS	EST.	
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REFERENCE	1 (bases 1 to 328)	
	AUTHORS Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Hayata, N., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Toya, T., Tsunoda, Y., Watanabe, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTs (Konno, H., et al.) Unpublished (2000)	
TITLE	JOURNAL	
	Unpublished (2000)	

REFERENCE	1 (bases 1 to 333)	266	CCCTGTGAGGAAGTAAGTGT 284
AUTHORS	Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Iehii,Y., Iehikawa,J., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.		
TITLE	RIKEN Mouse ESTs (Konno.H., et al.)		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/ Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh,M., Kitsuunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999) Please visit our web site (http://genome.rtc.riken.go.jp) for further details.		
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	/clone_lib="RIKEN full-length enriched, 12 days embryo eyeball"		
	/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5] GAGAGAGAGCGCGCACTCGAGTTTTTTTTTTTTTTTNN 3', cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5] GAGAGAGATTCGAGTTAATTAATTAATCCGCCCCCCC 3'. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC 1."		
ORIGIN			
Query Match	81.0%; Score 17; DB 2; Length 333;		
Best Local Similarity	89.5%; Pred. No. 1.8e+03;		
Matches	17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;		
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RESULT 40			
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DEFINITION	BB161894 RIKEN full-length enriched, 16 days neonate thymus Mus musculus cDNA clone A130064A09 3', mRNA sequence.		
ACCESSION	BB161894		
VERSION	BB161894.1		
KEYWORDS	GI:8817834		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 340)		
	Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.		
TITLE	RIKEN Mouse ESTs (Konno.H., et al.)		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/ Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh,M., Kitsuunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999) Please visit our web site (http://genome.rtc.riken.go.jp) for further details.		
FEATURES	Location/Qualifiers		
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	/clone_lib="RIKEN full-length enriched, 16 days neonate thymus"		
	/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5]"		

GAGAGAGAGAGGATCCAGAGCTCTTTTTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATTCAGTTAATTAATATCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."	
ORIGIN	
Query Match	81.0%; Score 17; DB 1; Length 340;
Best Local Similarity	89.5%; Pred. No. 1.9e+03;
Matches	17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY	1 CCTGTGAGGAAGTCTGT 19 
Db	270 CCTGTGAGGAAGTCTGT 288 
RESULT 41	
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LOCUS	AMGNNUC:NRPI4-00056-G12-A W Rat pituitary (10472) Rattus norvegicus
DEFINITION	cDNA clone nrpi4-00056-g12 5', mRNA sequence.
ACCESSION	CB766373
VERSION	CB766373.1 GI:29854764
KEYWORDS	EST.
SOURCE	Rattus norvegicus (Norway rat)
ORGANISM	Rattus norvegicus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
AUTHORS	1 (bases 1 to 418)
TITLE	Angen EST Program.
JOURNAL	Angen Rat EST Program
COMMENT	Unpublished (2003) Contact: Dan Fitzpatrick Angen, Inc One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA Tel: 805 447-4881 Plate: 00056 row: g column: 12.
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Best Local Similarity	89.5%; Pred. No. 1.9e+03;
Matches	17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY	3 CTGTGAGGAAGTCTGTCT 21 
Db	362 CTGTGAGGAAGTCTGTCT 344 
RESULT 42	
A1848082/c	460 bp mRNA linear EST 15-JUL-1999
LOCUS	UI-M-AP1-agk-b-12-0-UI.s1 NIH BMAP_MST_N Mus musculus cDNA clone
DEFINITION	UI-M-AP1-agk-b-12-0-UI 3', mRNA sequence.
ACCESSION	A1848082
VERSION	A1848082.1 GI:5491988
KEYWORDS	EST.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
GAGAGAGAGGATCCAGAGCTCTTTTTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATTCAGTTAATTAATATCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."	
ORIGIN	
Query Match	81.0%; Score 17; DB 1; Length 460;
Best Local Similarity	89.5%; Pred. No. 1.9e+03;
Matches	17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY	3 CTGTGAGGAAGTCTGTCT 21 
Db	310 CTGTGAGGAAGTCTGTCT 292 
RESULT 43	
DE020245	501 bp DNA linear GSS 06-APR-2005
LOCUS	Branchiostoma floridae DNA, clone: CH302-032P18.R, genomic survey
DEFINITION	sequence.
ACCESSION	DE020245
VERSION	DE020245.1 GI:62263715
KEYWORDS	GSS.
SOURCE	Branchiostoma floridae (Florida lancelet)
ORGANISM	Branchiostoma floridae Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae; Branchiostoma.
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the normalized corpus striatum library cDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined.	
Seq primer:	M13 Forward
POLYA=	Yes.
FEATURES	Location/Qualifiers 1..460 /organism="Mus musculus" /mol_type="mRNA" /strain="CS7BL/6J" /db_xref="taxon:10090" /clone="UI-M-AP1-agk-b-12-0-UI" /dev_stage="27-32 days" /lab_host="DH10B (Life Technologies)" /clone_lib="NIH BMAP_MST_N" /note="Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The NIH BMAP_MST_N library is a normalized library constructed from mouse striatum. The tag is a string of 5 nucleotides present between the Not I site and the oligo-dT track. The library was constructed as described by Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996. Tissue provided by Ms. Annie Novakovich, Zivic-Miller Laboratories. TAG_TISSUE=corpus-striatum TAG_LIB=NIH_BMAP_MST_N TAG_SEQ=ACGGC"

```

REFERENCE
AUTHORS      Fujiyama,A., Toyoda,A., Hattori,M. and Sakaki,Y.
TITLE        BAC end sequences of CHORI-302 Amphioxus Library
JOURNAL      Published Only in Database (2005)
REFERENCE    2 (bases 1 to 501)
AUTHORS      Fujiyama,A.
TITLE        Direct Submission
JOURNAL      Submitted (31-MAR-2005) Asao Fujiyama, The Institute of Physical
              and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
              1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
              (E-mail:afujiyam@gsc.riken.jp, URL:http://hgp.gsc.riken.jp/,
              Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT      PRIMERS
              Sequencing : TJ
LIBRARY      Vector      : pTARBAC2.1
              R.Site 1   : EcoRI
              R.Site 2   : EcoRI
FEATURES     Location/Qualifiers
              1..501
                /organism="Branchiostoma floridae"
                /mol_type="genomic DNA"
                /db_xref="taxon:7739"
                /clone="CH302-032P18.R"
                /sex="male"
                /tissue_type="sperm"
                /clone_lib="CHORI0302 Amphioxus genomic BAC library"
                /note="common name:amphioxus"
ORIGIN
Query Match      81.0%; Score 17; DB 11; Length 501;
Best Local Similarity 89.5%; Pred. No. 2e+03;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAACTWCTGT 19
    |||||
Db 140 CCTGTGAGGAACTTCTGT 158

RESULT 44
LOCUS      BW801116
DEFINITION BW801116 Amphioxus Branchiostoma floridae mRNA linear EST 23-MAY-2005
            larva whole animal Branchiostoma floridae cDNA clone bblv020j14 5',
            mRNA sequence.
ACCESSION  BW801116
VERSION    BW801116.1 GI:66409332
KEYWORDS   Branchiostoma floridae (Florida lancelet)
SOURCE     Branchiostoma floridae
ORGANISM   Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
            Branchiostoma.
REFERENCE  1 (bases 1 to 511)
AUTHORS    Yu,J., Holland,L.Z., Shin-i,T., Kohara,Y., Satou,Y. and Satoh,N.
TITLE      Expressed genes in Branchiostoma floridae
JOURNAL    Unpublished (2005)
COMMENT    Contact: Tadao Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
FEATURES   Location/Qualifiers
            1..511
              /organism="Branchiostoma floridae"
              /mol_type="mRNA"
              /db_xref="taxon:7739"
              /clone="bblv020j14"
              /tissue_type="whole animal"
              /dev_stage="larva"
              /clone_lib="Amphioxus Branchiostoma floridae unpublished
              cDNA library, larva whole animal"

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ORIGIN
Query Match      81.0%; Score 17; DB 5; Length 511;
Best Local Similarity 89.5%; Pred. No. 2e+03;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAACTWCTGT 19
    |||||
Db 160 CCTGTGAGGAACTTCTGT 178

RESULT 45
LOCUS      CW315697
DEFINITION CW315697 514 bp DNA linear GSS 31-OCT-2004
            104 806 11472500 148 35828 066 Sorghum methylation filtered library
            (LibID: 104) Sorghum bicolor genomic clone 11472500, genomic survey
            sequence.
ACCESSION  CW315697
VERSION    CW315697.1 GI:55031885
KEYWORDS   GSS.
SOURCE     Sorghum bicolor (sorghum)
ORGANISM   Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE  1 (bases 1 to 514)
AUTHORS    Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
            Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K., Korf,I.F.,
            McVernamy,J., Smith,M., Holsman,H., Roe,B.A., Wiley,G., Korf,I.F.,
            Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddaloeh,J.A. and
            Martienssen,R.A.
TITLE      Sorghum genome sequencing by methylation filtration
JOURNAL    PLOS Biol. 3 (1), e13 (2005)
COMMENT    15660154
            Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Plate: 806 row: o column: 20
            Seq primer: SWfor Forward
            Class: methylation filtered
            High quality sequence stop: 514.
FEATURES   Location/Qualifiers
            1..514
              /organism="Sorghum bicolor"
              /mol_type="genomic DNA"
              /cultivar="ATx623"
              /db_xref="taxon:4558"
              /clone="11472500"
              /clone_lib="Sorghum methylation filtered library (LibID:
              104)"
              /note="Organ: leaf; Vector: pBCSK(-); Site:1: HincII; DNA
              prepared from purified nuclei was randomly sheared,
              end-repaired, size fractionated to enrich for the 0.5 to 5
              kb fraction, ligated into HincII-digested pBCSK(-) vector
              and electroporated into E. coli cells. This is a
              methylation filtered library."
ORIGIN
Query Match      81.0%; Score 17; DB 10; Length 514;
Best Local Similarity 89.5%; Pred. No. 2e+03;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 CTGTGAGGAACTWCTGTCT 21
    |||||
Db 207 CTGTGAGGAACTACTGTTT 189

RESULT 46
LOCUS      DE024899
DEFINITION DE024899 542 bp DNA linear GSS 06-APR-2005

```

```

DEFINITION Branchiostoma floridae DNA, clone: CH302-039J07.F, genomic survey
sequence.
ACCESSION DE024899
VERSION DE024899.1 GI:62268369
KEYWORDS GSS
SOURCE Branchiostoma floridae (Florida lancelet)
ORGANISM Branchiostoma floridae
Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
Branchiostoma.
REFERENCE 1
AUTHORS Fujiyama, A., Toyoda, A., Hattori, M. and Sakaki, Y.
TITLE BAC end sequences of CHORI-302 Amphioxus Library
JOURNAL Published Only in Database (2005)
REFERENCE 2 (bases 1 to 542)
AUTHORS Fujiyama, A.
TITLE Direct Submission
JOURNAL Submitted (31-MAR-2005) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
(E-mail: afujiyam@gsc.riken.jp, URL: http://hgp.gsc.riken.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
PRIMERS
COMMENT Sequencing : T7
LIBRARY
Vector : pTARBAC2.1
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
Location/Qualifiers
1. .542
/organism="Branchiostoma floridae"
/mol_type="genomic DNA"
/db_xref="taxon:7739"
/clone="CH302-039J07.F"
/sex="male"
/tissue_type="sperm"
/clone_lib="CH0Ri0302 Amphioxus genomic BAC library"
/notes="common name: amphioxus"
FEATURES
source
Query Match 81.0%; Score 17; DB 11; Length 542;
Best Local Similarity 89.5%; Pred. No. 2e+03;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCCTGTGAGGAACTTCWTGT 19
128 CCCTGTGAGGATCTCTGT 146
Db
RESULT 47
LOCUS CO622122 546 bp mRNA linear EST 22-JUL-2004
DEFINITION DG9-226d2 DG9-ovary Canis familiaris cDNA 3', mRNA sequence.
ACCESSION CO622122
VERSION CO622122.1 GI:50525352
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
REFERENCE 1 (bases 1 to 546)
AUTHORS Schluter, T., Hermanns, J., Weindel, M., Schuette, D., Kranz, H.,
Henrich, J. and Loebebert, R.
TITLE Dog arrayTAG cDNA clone collection
JOURNAL Unpublished (2004)
COMMENT Contact: Thomas Schluter
LION Bioscience AG
Walhoferstrasse 98, D-69123 Heidelberg, Germany
Tel: +49 6221 4038 150
Fax: +49 6221 4038 290
Email: Thomas.Schluter@lionbioscience.com.
Location/Qualifiers
1. .546
/organism="Canis familiaris"
/mol_type="mRNA"
/strain="beagle"
/db_xref="taxon:9615"
/clone="CLN2496029"
/tissue_type="thyroid"
/lab_host="DH10B"
/clone_lib="LIB3578"
/notes="Vector: pSPORT1; Site_1: SalI; Site_2: NotI;
Control dog thyroid size selected"
FEATURES
source
Query Match 81.0%; Score 17; DB 8; Length 546;
Best Local Similarity 85.0%; Pred. No. 2e+03;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 CCCTGTGAGGAACTTCWTGTC 20
119 CCNTGTGAGGAATTCGTGC 100
Db
RESULT 49
LOCUS CA883299 547 bp mRNA linear EST 20-DEC-2002
DEFINITION B0102D04-3N NIA Mouse Neural Stem Cell (Differentiated) cDNA
Library (long) Mus musculus cDNA clone NIA: B0102D04 IMAGE: 30094023
3', mRNA sequence.
ACCESSION CA883299
VERSION CA883299.1 GI:27334848
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORIGIN
Query Match 81.0%; Score 17; DB 7; Length 546;
Best Local Similarity 89.5%; Pred. No. 2e+03;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCTGTGAGGAACTTCWTGT 19
338 CCTCTGAGGAATTCGTGT 356
Db
RESULT 48
LOCUS DN349087/c 546 bp mRNA linear EST 04-MAR-2005
DEFINITION LIB3578-029-Q1-K1-C5 LIB3578 Canis familiaris cDNA clone
DN349087
ACCESSION DN349087
VERSION DN349087.1 GI:60521779
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
REFERENCE 1 (bases 1 to 546)
AUTHORS Staten, N.R.
TITLE Direct Submission (Staten, N.R.)
JOURNAL Unpublished (2005)
COMMENT Contact: Nick Staten
Email: nicholas.r.staten@pfizer.com.
Location/Qualifiers
1. .546
/organism="Canis familiaris"
/mol_type="mRNA"
/strain="beagle"
/db_xref="taxon:9615"
/clone="CLN2496029"
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/lab_host="DH10B"
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/notes="Vector: pSPORT1; Site_1: SalI; Site_2: NotI;
Control dog thyroid size selected"
FEATURES
source
Query Match 81.0%; Score 17; DB 8; Length 546;
Best Local Similarity 85.0%; Pred. No. 2e+03;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 CCCTGTGAGGAACTTCWTGTC 20
119 CCNTGTGAGGAATTCGTGC 100
Db
RESULT 49
LOCUS CA883299 547 bp mRNA linear EST 20-DEC-2002
DEFINITION B0102D04-3N NIA Mouse Neural Stem Cell (Differentiated) cDNA
Library (long) Mus musculus cDNA clone NIA: B0102D04 IMAGE: 30094023
3', mRNA sequence.
ACCESSION CA883299
VERSION CA883299.1 GI:27334848
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
```

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ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS      Piao, Y., Dudekula, D.B., Qian, Y., Martin, P.R., Aiba, K., Vescovi, A.L.
and Ko, M.S.H.
TITLE        Systematic Analyses of NTA Mouse Neural Stem Cell (Differentiated)
JOURNAL      cDNA Library (Long)
COMMENT      Unpublished (2002)
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: B0102 row: D column: 04
Seq primer: -21M13 Forward
High quality sequence stop: 547
POLYA=Yes.

FEATURES
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1..547
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    /organism="Mus musculus"
    /mol_type="mRNA"
    /strain="CD1"
    /db_xref="nlaEST:B0102D04-3N"
    /db_xref="taxon:10090"
    /clone="NIA:B0102D04 IMAGE:30094023"
    /dev_stage="Adult"
    /lab_host="DH10B"
    /clone_lib="NIA Mouse Neural Stem Cell (Differentiated)
    cDNA Library (Long)"
    /note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2:
    NotI; Mouse cDNA project by the Laboratory of Genetics,
    National Institute on Aging (NIA), Intramural Research
    Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is
    a long-transcript enriched cDNA library (Ref. Genome Res.
    11: 1553-1558 (2001). [PMID: 11541991]. Total RNAs were
    obtained from Dr. Angelo L. Vescovi (Institute for Stem
    Cell Research, Italy). Double-stranded cDNAs were
    synthesized with an Oligo(dT) primer [Invitrogen:
    5'-pCAGTAGTCTAGATCGGCGGCGCCCTTTTCTTTT-3'] from
    2.0 Microgram of total RNA, treated with T4 DNA
    polymerase, and purified by ethanol-precipitation. The
    cDNAs were ligated to Lone-linker LL-Sal4, purified by
    phenol/chloroform, and separated from free linkers by
    Centricon 100. Then, the cDNAs were amplified by
    long-range high fidelity PCR using Ex Taq polymerase
    (Takara) with a primer Sal4-S. The products were purified
    by phenol/chloroform and Centricon 100. The cDNAs were
    digested with SalI and NotI enzymes and cloned into
    SalI/NotI site of pSPORT1 plasmid vector. The DH10B E.
    coli host was transformed with the ligation mixture by the
    standard chemical method. The average insert size is about
    3.2 kb. The library was constructed by Yulan Piao."

ORIGIN
Query Match      81.0%; Score 17; DB 6; Length 547;
Best Local Similarity 89.5%; Pred. No. 2e+03;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3  CTGTGAGGAACCTCTGCT 21
      ||| ||||| ||||| |||||
DB      238 CTGTAGGAACCTCTGCT 256

RESULT 50
AQ924133
LOCUS
DEFINITION
  AQ924133 556 bp DNA linear GSS 21-DEC-1999
  RPCI-23-294M20.TJ RPCI-23 Mus musculus genomic clone
  RPCI-23-294M20, genomic survey sequence.
ACCESSION
  AQ924133
VERSION
  AQ924133.1 GI:6613136
KEYWORDS
  GSS.

```

```

SOURCE
ORGANISM      Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS      Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S.,
Akinret, B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de
Jong, P. and Fraser, C.M.
TITLE        Mouse BAC End Sequences from Library RPCI-23
JOURNAL      Unpublished (1999)
COMMENT      Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac/ends/mouse/bac_end_intro.html
Plate: 294 row: M column: 20
Seq primer: SP6
Class: BAC ends.

FEATURES
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1..556
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    /mol_type="genomic DNA"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="RPCI-23-294M20"
    /sex="Female"
    /lab_host="DH10B"
    /clone_lib="RPCI-23"
    /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1:
    EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or
    brain genomic DNA was isolated and partially digested
    with a combination of EcoRI and EcoRI Methylase. Size
    selected DNA was cloned into the pBACe3.6 vector at the
    EcoRI sites. The ligation products were transformed into
    DH10B electrocompetent cells (BRL Life Technologies)."

ORIGIN
Query Match      81.0%; Score 17; DB 9; Length 556;
Best Local Similarity 89.5%; Pred. No. 2e+03;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2  CCTGTGAGGAACCTCTGTC 20
      ||| ||||| ||||| |||||
DB      233 CCTGTGAGGAACCTCTGTC 251

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Search completed: January 27, 2006, 07:06:29  
 Job time : 1562.5 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 27, 2006, 03:51:38 ; Search time 218.5 Seconds  
(without alignments)  
640.543 Million cell updates/sec

Title: US-10-070-415A-1

Perfect score: 21  
Sequence: 1 cccgtgagggaactwtgtct 21

Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 496997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : N\_Geneseq\_21:\*  
1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002as:\*  
7: Geneseqn2002bs:\*  
8: Geneseqn2003as:\*  
9: Geneseqn2003bs:\*  
10: Geneseqn2003cs:\*  
11: Geneseqn2003ds:\*  
12: Geneseqn2004as:\*  
13: Geneseqn2004bs:\*  
14: Geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20.6	98.1	21	10 ABX08667	Abx08667 Pathogeni
C 2	20.6	98.1	21	12 ADJ38963	Adj38963 Hepatitis
C 3	20.6	98.1	21	14 ADY75041	Ady75041 Hepatitis
4	20.6	98.1	23	12 ADJ38943	Adj38943 Hepatitis
5	20.6	98.1	23	14 ADY75021	Ady75021 Hepatitis
6	20.6	98.1	24	2 AAX60947	Aax60947 Hepatitis
7	20.6	98.1	24	6 ABX88459	Abx88459 Hepatitis
8	20.6	98.1	25	3 AAZ99212	Aaz99212 Primer fo
9	20.6	98.1	25	13 ADS34692	Ads34692 Primer Ds
10	20.6	98.1	27	2 AAT05212	Aat05212 Hepatitis
C 11	20.6	98.1	27	4 AAH44980	Aah44980 HCV speci
12	20.6	98.1	27	4 AAH75858	Aah75858 Mycobacte
13	20.6	98.1	27	6 ABN79962	Abn79962 Hepatitis
14	20.6	98.1	28	2 AAT05239	Aat05239 Hepatitis
15	20.6	98.1	28	3 AAZ57748	Aaz57748 Hepatitis
C 16	20.6	98.1	28	3 AAZ57779	Aaz57779 Hepatitis
17	20.6	98.1	28	14 ADV04753	Adv04753 Synthetic
18	20.6	98.1	28	14 ADV04766	Adv04766 Synthetic
19	20.6	98.1	28	14 ADV04766	Adv04766 Synthetic

C 20	20.6	98.1	45	2 AAT09176	Aat09176 Hepatitis
C 21	20.6	98.1	45	2 AAV20717	Aav20717 Hepatitis
C 22	20.6	98.1	45	2 AAV05026	Aav05026 Probe PA
C 23	20.6	98.1	45	2 AAV22769	Aav22769 Capture/A
C 24	20.6	98.1	45	2 ABK86838	Abk86838 Hepatitis
C 25	20.6	98.1	45	8 AAD56315	Aad56315 Hepatitis
C 26	20.6	98.1	45	12 ADQ74915	Adq74915 HCV Captu
C 27	20.6	98.1	45	14 AEB17467	Aeb17467 HCV 5'UTR
C 28	20.6	98.1	45	14 AEB54511	Aeb54511 HCV detec
C 29	20.6	98.1	51	2 AAO533262	Aao533262 Hepatitis
C 30	20.6	98.1	67	3 AAZ57776	Aaz57776 Hepatitis
C 31	20.6	98.1	70	13 ADW39164	Adw39164 Novel nuc
C 32	20.6	98.1	73	6 AAL40115	Aal40115 Pathogeni
C 33	20.6	98.1	79	13 ADW39166	Adw39166 Novel nuc
C 34	20.6	98.1	80	12 ADP20411	Adp20411 Hepatitis
C 35	20.6	98.1	85	6 AAD333033	Aad333033 HCV-s1 ov
C 36	20.6	98.1	95	13 ADW39165	Adw39165 Novel nuc
C 37	20.6	98.1	103	13 ADRO5701	Adro5701 Hepatitis
C 38	20.6	98.1	110	12 ADP87783	Adp87783 Hepatitis
C 39	20.6	98.1	127	6 ABX03545	Abx03545 Hepatitis
C 40	20.6	98.1	131	14 ADW15169	Adw15169 HCV H77C
C 41	20.6	98.1	131	14 ADW15171	Adw15171 HCV from
C 42	20.6	98.1	131	14 ADW15170	Adw15170 HCV from
C 43	20.6	98.1	131	14 ADW15174	Adw15174 HCV from
C 44	20.6	98.1	131	14 ADW15172	Adw15172 HCV from
C 45	20.6	98.1	131	14 ADW15173	Adw15173 HCV from
C 46	20.6	98.1	133	3 AAZ57175	Aaz57175 Human hep
C 47	20.6	98.1	155	3 AAZ57775	Aaz57775 Hepatitis
C 48	20.6	98.1	210	13 ADRO5716	Adro5716 Hepatitis
C 49	20.6	98.1	235	13 ADRO5719	Adro5719 Hepatitis
C 50	20.6	98.1	242	3 AAZ37774	Aaz37774 Cloned HC
C 51	20.6	98.1	260	3 AAZ57774	Aaz57774 Hepatitis
C 52	20.6	98.1	265	14 ADW15166	Adw15166 HCV RT-PC
C 53	20.6	98.1	266	14 ADW15165	Adw15165 HCV H77C
C 54	20.6	98.1	267	6 ABN79975	Abn79975 Hepatitis
C 55	20.6	98.1	278	6 ABN79973	Abn79973 Hepatitis
C 56	20.6	98.1	290	13 ADRO5722	Adro5722 Hepatitis
C 57	20.6	98.1	297	4 AAH75861	Aah75861 Mycobacte
C 58	20.6	98.1	299	10 AAD55565	Aad55565 IG57272 H
C 59	20.6	98.1	305	2 AAT87088	Aat87088 HCV ampli
C 60	20.6	98.1	305	6 ABN79971	Abn79971 Hepatitis
C 61	20.6	98.1	305	6 ABN79969	Abn79969 Hepatitis
C 62	20.6	98.1	305	6 ABN79972	Abn79972 Hepatitis
C 63	20.6	98.1	305	6 ABN79970	Abn79970 Hepatitis
C 64	20.6	98.1	305	6 ABN79974	Abn79974 Hepatitis
C 65	20.6	98.1	306	2 AAG67079	Aag67079 Hepatitis
C 66	20.6	98.1	308	3 AAZ75294	Aaz75294 Novel hep
C 67	20.6	98.1	308	12 ADN35973	Adn35973 HCV cDNA
C 68	20.6	98.1	310	6 ABK70877	Abk70877 HCV genom
C 69	20.6	98.1	312	3 AAZ36198	Aaz36198 Adapted H
C 70	20.6	98.1	314	3 AAZ36197	Aaz36197 Adapted H
C 71	20.6	98.1	323	6 ABK70883	Abk70883 HCV genom
C 72	20.6	98.1	323	6 ABK70882	Abk70882 HCV genom
C 73	20.6	98.1	323	14 ADX58606	Adx58606 Bacteriop
C 74	20.6	98.1	326	6 ABK70880	Abk70880 HCV genom
C 75	20.6	98.1	327	3 AAZ36199	Aaz36199 Adapted H
C 76	20.6	98.1	327	6 ABK70884	Abk70884 HCV genom
C 77	20.6	98.1	328	6 ABL46276	Abi46276 Hepatitis
C 78	20.6	98.1	328	6 ABL46275	Abi46275 Hepatitis
C 79	20.6	98.1	328	6 ABL46278	Abi46278 Hepatitis
C 80	20.6	98.1	328	6 ABL46273	Abi46273 Hepatitis
C 81	20.6	98.1	328	8 AAL53724	Aal53724 Hepatitis
C 82	20.6	98.1	328	8 AAD49656	Aad49656 Human int
C 83	20.6	98.1	329	6 ABK70871	Abk70871 HCV genom
C 84	20.6	98.1	332	2 AAG75226	Aag75226 Hepatitis
C 85	20.6	98.1	332	6 ABK70878	Abk70878 HCV genom
C 86	20.6	98.1	333	6 ABK70881	Abk70881 HCV genom
C 87	20.6	98.1	333	6 ABK70867	Abk70867 HCV genom
C 88	20.6	98.1	333	6 ABK70879	Abk70879 HCV genom
C 89	20.6	98.1	333	6 ABK70876	Abk70876 HCV genom
C 90	20.6	98.1	334	2 AAG98272	Aag98272 Hepatitis
C 91	20.6	98.1	334	6 ABK70869	Abk70869 HCV genom
C 92	20.6	98.1	335	6 ABK70868	Abk70868 HCV genom

93 20.6 98.1 335 6 ABK70885 Abk70885 HCV genom  
94 20.6 98.1 336 6 ABK70874 Abk70874 HCV genom  
95 20.6 98.1 337 6 ABK70870 Abk70870 HCV genom  
96 20.6 98.1 338 13 ADR05731 ADR05731 Hepatitis  
97 20.6 98.1 339 13 ADR05688 ADR05688 Hepatitis  
98 20.6 98.1 340 6 ABK70886 Abk70886 HCV genom  
99 20.6 98.1 340 14 ADV04744 ADV04744 Synthetic  
100 20.6 98.1 340 14 ADV04743 ADV04743 Synthetic

ALIGNMENTS

RESULT 1  
ABX08657  
ID ABX08667 standard; DNA; 21 BP.  
XX  
AC ABX08667;  
XX  
DT 20-JAN-2003 (first entry)  
XX  
DE Pathogenic organism detection method associated PCR primer #1.  
XX  
KW PCR; primer; ss; hepatitis C virus; human; pathogenic microorganism;  
KW influenza; AIDS; acquired immunodeficiency syndrome.  
XX  
OS Hepatitis C virus.  
XX  
PN WO20027281-A1.  
XX  
PD 03-OCT-2002.  
XX  
PF 05-MAR-2002; 2002WO-JF002030.  
XX  
PR 27-MAR-2001; 2001JP-00090053.  
PR 18-SEP-2001; 2001JP-00284112.  
XX  
PA (TOKE ) TOSHIBA KK.  
XX  
PI Hashimoto K, Hashimoto M, Mishiro S, Oota Y;  
XX  
XX WPI; 2003-040593/03.  
XX  
PT Detecting nucleic acids relating diseases particularly due to pathogenic  
PT microorganisms e.g. hepatitis, influenza and AIDS in individuals from  
PT their data using immobilized probes on substrate, also for therapeutic  
PT evaluation.  
XX  
PS Claim 16; Page 83; 125pp; Japanese.  
XX  
CC This invention relates to a method for obtaining first data on a nucleic  
CC acid from an individual exposed to a specific disease and second data on  
CC a nucleic acid from a pathogenic microorganism occurring in the  
CC individual in order to relate the specific disease to such pathogenic  
CC microorganism. The method of the invention comprises the reaction of a  
CC nucleic acid extract from the individual with a probe-immobilization  
CC substrate containing first and second probes for detection of the  
CC pathogenic microorganism with the first probe to relate to the specific  
CC microbe-caused disease, and the second probe for detecting a specific  
CC nucleic acid in the individual and obtaining first data from the reaction  
CC results as well as the detected binding of a nucleic acid with the first  
CC probe and/or second data from the detected binding of a nucleic acid with  
CC the second probe. The method of the invention is useful for detecting  
CC nucleic acids relating diseases particularly due to pathogenic  
CC microorganisms e.g. hepatitis C, influenza and AIDS in individuals, and  
CC also for therapeutic evaluation. Such a method is convenient and accurate  
CC and may be used to design specific therapy for effective treatment even  
CC for individual patients in a tailor-made manner. The present sequence  
CC represents a PCR primer used in the method of the invention  
XX  
SQ Sequence 21 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 1 Other;  
Query Match 98.1%; Score 20.6; DB 10; Length 21;

Best Local Similarity 100.0%; Pred. No. 3.2;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CCCTGTGAGGAACACTWCTGTCT 21  
DB 1 CCCTGTGAGGAACACTWCTGTCT 21  
RESULT 2  
ADJ38963/c  
ID ADJ38963 standard; RNA; 21 BP.  
XX  
AC ADJ38963;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Hepatitis C virus siRNA antisense oligonucleotide 5U8.  
XX  
KW small interfering RNA; siRNA; modified ribonucleotide;  
KW viral replication inhibition; hepatitis C virus; HCV; hepatitis C;  
KW antiinflammatory; hepatotropic; virucide; hepatitis A virus;  
KW hepatitis D virus; hepatitis E virus; Ebola virus; influenza virus;  
KW rotavirus; reovirus; retrovirus; poliovirus; human papilloma virus;  
KW metapneumoniavirus; coronavirus; viral infection; ss.  
XX  
OS Hepatitis C virus.  
OS Synthetic.  
XX  
PN WO2004011647-A1.  
XX  
PD 05-FEB-2004.  
XX  
PF 25-JUL-2003; 2003WO-US023104.  
XX  
PR 26-JUL-2002; 2002US-0398605P.  
XX  
PA (CHIR ) CHIRON CORP.  
XX  
PI Han J, Seo MY, Houghton M;  
XX  
XX WPI; 2004-143862/14.  
XX  
PT New RNase resistant small interfering RNA, useful for treating viral  
PT infections, e.g., hepatitis C, influenza virus or coronavirus infection.  
XX  
PS Example 12; Fig 2; 74pp; English.  
XX  
CC The present invention describes a small interfering RNA (siRNA) which  
CC comprises a modified ribonucleotide, where the siRNA is resistant to  
CC RNase and retains the ability to inhibit viral replication. Also  
CC described: (1) inactivating a virus in a patient; (2) making a modified  
CC siRNA that targets a nucleic acid sequence in a virus; (3) a double-  
CC stranded RNA molecule of 10-30 nucleotides that inhibits replication of  
CC hepatitis C virus (HCV); (4) inducing targeted RNA interference toward  
CC HCV in hepatic cells; (5) inhibiting replication of HCV; (6) a vector  
CC comprising a DNA segment encoding the RNA molecule; (7) a host cell  
CC comprising the vector of (6); (8) inhibiting replication of HCV in cells  
CC carrying HCV; (9) treating hepatitis C in a subject; (10) a modified  
CC siRNA molecule comprising a double-stranded RNA molecule of 10-30  
CC nucleotides in length, which mediates RNA interference toward a target  
CC agent or virus and is linked to at least one receptor-binding ligand; and  
CC (11) inducing targeted RNA interference in a patient. The modified siRNA  
CC molecules have antiinflammatory, hepatotropic and virucide activities.  
CC The modified RNA molecules are useful for inactivating virus in mammalian  
CC cells. The siRNAs are useful for treating hepatitis C virus, hepatitis A  
CC virus, hepatitis D virus, hepatitis E virus, Ebola virus, influenza  
CC virus, rotavirus, reovirus, retrovirus, poliovirus, human papilloma  
CC virus, metapneumoniavirus or coronavirus infections. The methods of the  
CC invention can be used to correct or compensate for cellular physiological  
CC abnormalities involved in conferring susceptibility to viral infections.  
CC in patients and/or alleviate symptoms of a viral infection in patients.  
CC The present sequence represents an siRNA oligonucleotide, which is used  
CC in an example from the present invention.

XX SQ Sequence 21 BP; 6 A; 5 C; 6 G; 0 T; 4 U; 0 Other;  
Query Match 98.1%; Score 20.6; DB 12; Length 21;  
Best Local Similarity 95.2%; Pred. No. 3.2;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCCTGTGAGGAAGTCTGTCT 21  
|||||:|||||:|||||  
Db 21 CCCTGTGAGGAAGTCTGTCT 1

RESULT 3  
ADY75041/c  
ID ADY75041 standard; RNA; 21 BP.  
XX AC ADY75041;  
XX DT 02-JUN-2005 (first entry)  
XX DE Hepatitis C virus antisense siRNA5U8 oligo targeted to 5' UTR Seq 30.  
XX KW virus inactivation: RNA interference; short interfering RNA; siRNA;  
XX KW gene silencing; gene therapy; antiinflammatory; hepatotropic; virucide;  
XX KW viral infection; hepatitis C virus infection; ss;  
XX KW antisense oligonucleotide.  
XX OS Hepatitis C virus.  
XX US2005058982-A1.  
XX PN 17-MAR-2005.  
XX PD 25-JUL-2003; 2003US-00626879.  
XX PF 26-JUL-2002; 2002US-0398605P.  
XX PR 11-APR-2003; 2003US-0461838P.  
XX PR 14-MAY-2003; 2003US-0470230P.  
XX PA (CHIR ) CHIRON CORP.  
XX PI Han J, Seo M, Houghton M;  
XX WPI; 2005-222217/23.  
XX DR  
XX PT Inactivating a virus (e.g. HCV) in a patient to treat the viral infection  
XX PT comprises administering to the patient a modified small interfering RNA  
XX PT in an amount to inactivate the virus.  
XX PS Disclosure; SEQ ID NO 30; 60pp; English.  
XX CC This invention relates to a novel method for inactivating a virus in a  
XX CC patient. Specifically, it refers to the administration of a modified  
XX CC small interfering RNA (siRNA) in an amount suitable to inactivate the  
XX CC virus, where the siRNA comprises a modified ribonucleotide that is  
XX CC resistant to RNase and retains the ability to inhibit viral replication.  
XX CC In particular, it refers to double-stranded RNA (dsRNA) molecules of  
XX CC about 10-30 nucleotides in length that can inhibit replication of the  
XX CC hepatitis C virus (HCV) by gene specific suppression of expression,  
XX CC especially in hepatic cells. The present invention, however, also  
XX CC describes the inactivation of a virus chosen from hepatitis A virus,  
XX CC hepatitis B virus, hepatitis D virus, hepatitis E virus, Ebola virus,  
XX CC influenza virus, rotavirus, reovirus, retrovirus, poliovirus, human  
XX CC papilloma virus, metapneumovirus or coronavirus. The siRNA is prepared by  
XX CC identifying a target nucleotide sequence in a virus genome that is  
XX CC necessary for replication and producing a 2' modified siRNA that will  
XX CC bind to this region, where the 2' modification is chosen from fluoro-,  
XX CC methyl-, methoxyethyl- or propyl-modification. As such, these siRNA  
XX CC molecules and compositions derived thereof can be used in gene therapy  
XX CC and exhibit antiinflammatory, hepatotropic and virucide activities. The  
XX CC composition and methods are useful for treating viral infections, such as  
XX CC HCV infections. This oligonucleotide sequence is a Hepatitis C virus  
XX CC siRNA oligo of the invention.

XX SQ Sequence 21 BP; 6 A; 5 C; 6 G; 0 T; 4 U; 0 Other;  
Query Match 98.1%; Score 20.6; DB 14; Length 21;  
Best Local Similarity 95.2%; Pred. No. 3.2;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCCTGTGAGGAAGTCTGTCT 21  
|||||:|||||:|||||  
Db 21 CCCTGTGAGGAAGTCTGTCT 1

RESULT 4  
ADJ38943  
ID ADJ38943 standard; RNA; 23 BP.  
XX AC ADJ38943;  
XX DT 06-MAY-2004 (first entry)  
XX DE Hepatitis C virus siRNA target oligonucleotide 5U8.  
XX KW small interfering RNA; siRNA; modified ribonucleotide;  
XX KW viral replication inhibition; hepatitis C virus; HCV; hepatitis C;  
XX KW antiinflammatory; hepatotropic; virucide; hepatitis A virus;  
XX KW hepatitis D virus; hepatitis E virus; Ebola virus; influenza virus;  
XX KW rotavirus; reovirus; retrovirus; poliovirus; human papilloma virus;  
XX KW metapneumovirus; coronavirus; viral infection; target; ss.  
XX OS Hepatitis C virus.  
XX OS Synthetic.  
XX PN WO2004011647-A1.  
XX XX 05-FEB-2004.  
XX PD 25-JUL-2003; 2003WO-US023104.  
XX PF 26-JUL-2002; 2002US-0398605P.  
XX PR (CHIR ) CHIRON CORP.  
XX PA Han J, Seo MY, Houghton M;  
XX WPI; 2004-143862/14.  
XX DR  
XX PT New RNase resistant small interfering RNA, useful for treating viral  
XX PT infections, e.g., hepatitis C, influenza virus or coronavirus infection.  
XX PS Example 12; Fig 2; 74pp; English.  
XX CC The present invention describes a small interfering RNA (siRNA) which  
XX CC comprises a modified ribonucleotide, where the siRNA is resistant to  
XX CC RNase and retains the ability to inhibit viral replication. Also  
XX CC described: (1) inactivating a virus in a patient; (2) making a modified  
XX CC siRNA that targets a nucleic acid sequence in a virus; (3) a double-  
XX CC stranded RNA molecule of 10-30 nucleotides that inhibits replication of  
XX CC hepatitis C virus (HCV); (4) inducing targeted RNA interference toward  
XX CC HCV in hepatic cells; (5) inhibiting replication of HCV; (6) a vector  
XX CC comprising a DNA segment encoding the RNA molecule; (7) a host cell  
XX CC comprising the vector of (6); (8) inhibiting replication of HCV in cells  
XX CC carrying HCV; (9) treating hepatitis C in a subject; (10) a modified  
XX CC siRNA molecule comprising a double-stranded RNA molecule of 10-30  
XX CC nucleotides in length, which mediates RNA interference toward a target  
XX CC agent or virus and is linked to at least one receptor-binding ligand; and  
XX CC (11) inducing targeted RNA interference in a patient. The modified siRNA  
XX CC molecules have antiinflammatory, hepatotropic and virucide activities.  
XX CC The modified RNA molecules are useful for inactivating virus in mammalian  
XX CC cells. The siRNAs are useful for treating hepatitis C virus, hepatitis A  
XX CC virus, hepatitis D virus, hepatitis E virus, Ebola virus, influenza  
XX CC virus, rotavirus, reovirus, retrovirus, poliovirus, human papilloma  
XX CC virus, metapneumovirus or coronavirus infections. The methods of the  
XX CC invention can be used to correct or compensate for cellular physiological

CC abnormalities involved in conferring susceptibility to viral infections  
CC in patients and/or alleviate symptoms of a viral infection in patients.  
CC The present sequence represents an siRNA target oligonucleotide, which is  
CC used in an example from the present invention.

XX  
SQ Sequence 23 BP; 4 A; 7 C; 5 G; 0 T; 7 U; 0 Other;

Query Match 98.1%; Score 20.6; DB 12; Length 23;  
Best Local Similarity 66.7%; Pred. No. 3.3;  
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAACACTWCTGTCT 21  
|||:|||||:|||||:|:|:  
Db 1 CCCUGUGAGGAACUACUGUCU 21

## RESULT 5

ADY75021  
ID ADY75021 standard; RNA; 23 BP.

XX  
AC ADY75021;

XX  
DT 02-JUN-2005 (first entry)

XX  
DE Hepatitis C virus RNA target of a viral inactivating siRNA duplex Seq 10.

XX  
KW virus inactivation; RNA interference; gene silencing; gene therapy;  
KW antiinflammatory; hepatotropic; virucide; viral infection;  
KW hepatitis C virus infection; ss.

XX  
OS Hepatitis C virus.

XX  
PN US2005058982-A1.

XX  
PD 17-MAR-2005.

XX  
PF 25-JUL-2003; 2003US-00626879.

XX  
PR 26-JUL-2002; 2002US-0398605P.

XX  
PR 11-APR-2003; 2003US-0461838P.

XX  
PR 14-MAY-2003; 2003US-0470230P.

XX  
PA (CHIR ) CHIRON CORP.

XX  
PI Han J, Seo M, Houghton M;

XX  
PP WPI; 2005-222217/23.

XX  
PT Inactivating a virus (e.g. HCV) in a patient to treat the viral infection  
PT comprises administering to the patient a modified small interfering RNA  
PT in an amount to inactivate the virus.

XX  
PS Disclosure; SEQ ID NO 10; 60pp; English.

XX  
CC This invention relates to a novel method for inactivating a virus in a  
CC patient. Specifically, it refers to the administration of a modified  
CC small interfering RNA (siRNA) in an amount suitable to inactivate the  
CC virus, where the siRNA comprises a modified ribonucleotide that is  
CC resistant to RNase and retains the ability to inhibit viral replication.  
CC In particular, it refers to double-stranded RNA (dsRNA) molecules of  
CC about 10-30 nucleotides in length that can inhibit replication of the  
CC hepatitis C virus (HCV) by gene specific suppression of expression,  
CC especially in hepatic cells. The present invention, however, also  
CC describes the inactivation of a virus chosen from hepatitis A virus,  
CC hepatitis B virus, hepatitis D virus, hepatitis E virus, Ebola virus,  
CC influenza virus, rotavirus, reovirus, retrovirus, poliovirus, human  
CC papilloma virus, metapneumovirus or coronavirus. The siRNA is prepared by  
CC identifying a target nucleotide sequence in a virus genome that is  
CC necessary for replication and producing a 2' modified siRNA that will  
CC bind to this region, where the 2' modification is chosen from fluoro-,  
CC methyl-, methoxyethyl- or propyl-modification. As such, these siRNA  
CC molecules and compositions derived thereof can be used in gene therapy  
CC and exhibit antiinflammatory, hepatotropic and virucide activities. The

CC composition and methods are useful for treating viral infections, such as  
CC HCV infections. This oligonucleotide sequence is a Hepatitis C virus RNA  
CC oligo, target of an siRNA duplex that inhibits viral replication, given  
CC in an exemplification of the invention.

XX  
SQ Sequence 23 BP; 4 A; 7 C; 5 G; 0 T; 7 U; 0 Other;

Query Match 98.1%; Score 20.6; DB 14; Length 23;  
Best Local Similarity 66.7%; Pred. No. 3.3;  
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAACACTWCTGTCT 21  
|||:|||||:|||||:|:|:  
Db 1 CCCUGUGAGGAACUACUGUCU 21

## RESULT 6

AAX60947  
ID AAX60947 standard; DNA; 24 BP.

XX  
AC AAX60947;

XX  
DT 16-AUG-1999 (first entry)

XX  
DE Hepatitis C virus (HCV) primer HCVC.

XX  
KW Nucleic acid detection; pathogen; bacteria; virus; hepatitis C virus;  
KW HCV; hepatitis B; HBV; hepatitis G; HGV; HIV; fungus; protozoa; ss;  
KW parasite; mycoplasma; genetic mutation; food contamination; PCR primer.

XX  
OS Synthetic.

XX  
OS Hepatitis C virus.

XX  
PN WO928503-A1.

XX  
PD 10-JUN-1999.

XX  
PF 16-NOV-1998; 98WO-US024494.

XX  
PR 03-DEC-1997; 97IT-RM000749.

XX  
PA (DIAS-) DIASORIN INT INC.

XX  
PI Primi D, Mantero G;

XX  
PP WPI; 1999-371139/31.

XX  
PT Detection of single-stranded polynucleotide analytes.

XX  
PS Claim 53; Page 65; 73pp; English.

XX  
CC The invention relates to a new method for detection of single-stranded  
CC (ss) polynucleotide analytes that comprises using ss polynucleotide  
CC probes which hybridize to the analyte and are bound to a solid support  
CC where double-stranded (ds) polynucleotides are detected. The method can  
CC be used for detecting ss PN analytes for the detection of pathogens such  
CC as bacteria, viruses such as hepatitis C (HCV), hepatitis B (HBV),  
CC hepatitis G (HGV), or HIV, fungi, protozoa, parasites or mycoplasma. The  
CC method can be used to detect the presence of genetic mutations which have  
CC diagnostic or prognostic value. Pathogen contamination of food and drink  
CC supplies can also be detected using the method. The method provides for  
CC the sensitive and specific detection of ss PN analytes at concentration  
CC as low as 0.1fg

XX  
SQ Sequence 24 BP; 4 A; 8 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 98.1%; Score 20.6; DB 2; Length 24;  
Best Local Similarity 95.2%; Pred. No. 3.3;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAACACTWCTGTCT 21  
|||:|||||:|||||:|:|:  
Db 2 CCCTGTGAGGAACACTGTGTCT 22

RESULT 7  
 ID ABK88459 standard; DNA; 24 BP.  
 AC ABK88459;  
 XX  
 DT 07-OCT-2002 (first entry)  
 XX  
 DE Hepatitis C virus forward PCR primer CTL1.f.  
 XX  
 KW HCV; PCR; primer; ss; CTL1.f; internal control; human parvovirus;  
 KW 5' nuclease polymerase chain reaction assay; hepatitis A virus;  
 KW human immunodeficiency virus; hepatitis B virus.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN WO200252041-A2.  
 XX  
 PD 04-JUL-2002.  
 XX  
 PF 19-DEC-2001; 2001WO-EP015069.  
 XX  
 PR 22-DEC-2000; 2000US-00746874.  
 XX  
 PA (BAXT ) BAXTER AG.  
 XX  
 PI Gessner M;  
 XX  
 DR WPI; 2002-575389/61.  
 XX  
 PT 5' nuclease polymerase chain reaction assay, useful for detecting  
 PT pathogens, e.g. HIV or hepatitis virus, comprises employing an internal  
 PT control probe having a nucleic acid to the inverted target  
 PT oligonucleotide probe binding site.  
 XX  
 PS Example 1; Page 23; 37pp; English.  
 XX  
 CC The invention relates to a 5' nuclease polymerase chain reaction (PCR)  
 CC assay having an internal control comprising an oligonucleotide having as  
 CC part of its sequence an inverse of a target oligonucleotide probe binding  
 CC site nucleic acid sequence, and an internal control probe having a  
 CC nucleic acid sequence complementary to the inverted target  
 CC oligonucleotide probe binding site. Also included is a hepatitis C virus  
 CC (HCV) 5' nuclease PCR assay comprising: (a) a first probe having a first  
 CC detectable label and a nucleic acid sequence complementary to a target  
 CC HCV oligonucleotide probe binding sequence; (b) a 5' nuclease enzyme; (c)  
 CC a second probe having a second detectable label and having a nucleic acid  
 CC sequence complementary to an internal standard oligonucleotide probe  
 CC binding sequence, where the internal standard oligonucleotide probe  
 CC binding sequence is the inverse of the target HCV oligonucleotide probe  
 CC binding sequence; (d) at least one primer complementary to primer binding  
 CC sites on the target HCV nucleotide and the internal standard  
 CC oligonucleotide; and (e) at least one primer complementary to primer  
 CC binding sites on the target HCV nucleotide. The 5' nuclease PCR assay is  
 CC useful for detecting pathogens such as human immunodeficiency viruses  
 CC (HIV), hepatitis C virus, hepatitis B virus, human parvovirus and  
 CC hepatitis A virus, as well as non-viral pathogens. The method is also  
 CC used for quick and accurate determination of optimum nucleic acid  
 CC sequences for use as internal amplification controls in 5' nuclease PCR  
 CC assays. The internal control is used to detect nucleic acid amplification  
 CC assay corruption, and to verify assay performance. The present sequence  
 CC is an HCV PCR primer used to demonstrate the method of the invention  
 XX  
 SQ Sequence 24 BP; 5 A; 7 C; 5 G; 7 T; 0 U; 0 Other;  
 Query Match 98.1%; Score 20.6; DB 6; Length 24;  
 Best Local Similarity 95.2%; Pred. No. 3.3;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CCCTGTGAGGAAGTCTGTCT 21  
 |||||  
 RESULT 8  
 ID AAZ99212 standard; DNA; 25 BP.  
 AC AAZ99212;  
 XX  
 DT 19-JUN-2000 (first entry)  
 XX  
 DE Primer for primer-specific and mispair extension analysis of HCV.  
 XX  
 KW Primer-specific and mispair extension assay; PSMEA;  
 KW genotype determination; HCV; gene variation; PCR primer; ss.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN WO200009745-A1.  
 XX  
 PD 24-FEB-2000.  
 XX  
 PF 09-AUG-1999; 99WO-CA000733.  
 XX  
 PR 13-AUG-1998; 98CA-02245039.  
 XX  
 PA (CABL-) CANADIAN BLOOD SERVICES.  
 PA (HEMA-) HEMA-QUEBEC.  
 XX  
 PI Hu Y;  
 XX  
 DR WPI; 2000-224367/19.  
 XX  
 PT Primer-specific and mispair extension assay for identifying gene  
 PT variations, comprises specific primer amplification of unknown nucleic  
 PT acid sequences of patients using incomplete dNTP sets.  
 XX  
 PS Disclosure; Page 13; 65pp; English.  
 XX  
 CC AAZ99212-26 represent PCR primers used in a primer-specific and mispair  
 CC extension assay (PSMEA) for genotype determination of Hepatitis C virus  
 CC (HCV). The method comprises extending an unknown nucleic acid sequence  
 CC (from a patient) using a primer specific for particular genotype and  
 CC incomplete set of dNTPs under suitable conditions followed by  
 CC characterizing and comparing the extension products with known nucleic  
 CC acid sequences of various genotypes. The present primers are used for  
 CC detecting nucleotide variations in the 5' untranslated region of the HCV  
 CC genome. PSMEA is capable of accurately detecting heterozygotes and  
 CC nucleotide mutations in a nucleic acid sequence. The PSMEA is useful for  
 CC identifying gene variations such as in different genotypes or subtypes of  
 CC a given genotype, especially Hepatitis C virus genotypes and subtypes  
 XX  
 SQ Sequence 25 BP; 4 A; 8 C; 5 G; 8 T; 0 U; 0 Other;  
 Query Match 98.1%; Score 20.6; DB 3; Length 25;  
 Best Local Similarity 95.2%; Pred. No. 3.3;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CCCTGTGAGGAAGTCTGTCT 21  
 |||||  
 DB 4 CCCTGTGAGGAAGTCTGTCT 24  
 |||||  
 RESULT 9  
 ID ADS34692 standard; DNA; 25 BP.  
 AC ADS34692;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Primer Ds5-41-S25, seq id 35.  
 XX  
 SQ Sequence 24 BP; 5 A; 7 C; 5 G; 7 T; 0 U; 0 Other;  
 Query Match 98.1%; Score 20.6; DB 6; Length 24;  
 Best Local Similarity 95.2%; Pred. No. 3.3;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CCCTGTGAGGAAGTCTGTCT 21  
 |||||

KW Virucide; antiinflammatory; hepatotropic; hepatitis C virus; HCV;  
 KW proliferation; siRNA; short interfering RNA; RNA interference;  
 KW gene silencing; PCR; primer; ss.  
 XX  
 XX Unidentified.  
 OS  
 PN WO2004078974-A1.  
 XX  
 XX 16-SEP-2004.  
 PD  
 XX 23-JAN-2004; 2004WO-JP000605.  
 PF  
 XX 24-JAN-2003; 2003JP-00016750.  
 XX  
 XX (TOKM-) TOKYO METROPOLITAN ORG MEDICAL RES.  
 PA (CHUS) CHUGAI SEIYAKU KK.  
 XX  
 XX Kohara M, Watanabe T, Taira K, Miyagishi M, Sudo M;  
 PI WPI; 2004-662428/64.  
 XX  
 DR New oligo ribonucleotide or peptide nucleic acid capable of sequence-  
 XX specifically binding with RNA of hepatitis C virus, useful for inhibiting  
 PT proliferation of hepatitis C virus and useful as hepatitis C virus  
 PT therapeutic agent.  
 XX  
 XX Example 6; SEQ ID NO 35; 80pp; Japanese.  
 PS  
 XX The invention relates to an oligo ribonucleotide or peptide nucleic acid  
 CC (I) capable of sequence-specifically binding with RNA of hepatitis C  
 CC virus (HCV), and comprising a sequence hybridising under stringent  
 CC conditions with RNA of HCV. The method of the invention relates to the  
 CC inhibition of the proliferation of HCV. The oligo ribonucleotide or  
 CC peptide nucleic acid of the invention is useful for inhibiting the  
 CC proliferation of HCV which involves contacting (I) with RNA of HCV. (I)  
 CC is useful as a therapeutic agent of hepatitis C. The current sequence  
 CC represents a primer used in an example from the invention.  
 XX  
 XX Sequence 25 BP; 5 A; 8 C; 5 G; 7 T; 0 U; 0 Other;  
 SQ  
 Query Match 98.1%; Score 20.6; DB 13; Length 25;  
 Best Local Similarity 95.2%; Pred. No. 3.3;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CCCTGTGAGGAAGTCTGCTCT 21  
 Db 5 CCCTGTGAGGAAGTCTGCTCT 25  
 RESULT 10  
 AAQ68058  
 ID AAQ68058 standard; DNA; 27 BP.  
 XX  
 XX AAQ68058;  
 AC  
 XX 25-MAR-2003 (revised)  
 DT 19-DEC-1994 (first entry)  
 DT  
 XX  
 XX Primer HcPr98 for HCV genotyping (universal).  
 DE  
 XX Hepatitis C virus; HCV; probe; genotyping; hybridisation;  
 KW non-A, non-B hepatitis; NANBH; amplification; primer;  
 KW polymerase chain reaction; PCR; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX WO9412670-A2.  
 PN  
 XX 09-JUN-1994.  
 PD  
 XX 26-NOV-1993; 93WO-EP003325.  
 PF  
 XX 27-NOV-1992; 92EP-00403222.  
 PR

PR 31-AUG-1993; 93EP-00402129.  
 XX (INNO-) INNOGENETICS NV SA.  
 PA  
 PI Maertens G, Stuyver L, Rossau R, Van Heuverswyn H;  
 XX WPI; 1994-200296/24.  
 DR  
 XX Process for genotyping Hepatitis C virus (HCV) isolates - utilises probes  
 PT hybridising to HCV isolate domains.  
 PT  
 XX Claim 13; Page 73; 96pp; English.  
 PS  
 XX Genotyping HCV utilises probes hybridising to HCV isolate domains. HCV  
 CC types 2, 3, 4, 5 or 6 and subtypes 1a, 1b, 2a, 2b, 3a, 3b, 3c, 4a, 4b,  
 CC 4c, 4d, 4e, 4f, 4g and 4h can be typed. The hybridisation step is pref.  
 CC preceded by an amplification step (PCR) using universal primers given in  
 CC AAQ68058-61. (Updated on 25-MAR-2003 to correct PN field.)  
 CC  
 XX Sequence 27 BP; 4 A; 9 C; 6 G; 7 T; 0 U; 1 Other;  
 SQ  
 Query Match 98.1%; Score 20.6; DB 2; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 3.3;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CCCTGTGAGGAAGTCTGCTCT 21  
 Db 1 CCCTGTGAGGAAGTCTGCTCT 21  
 RESULT 11  
 AAQ68058  
 ID AAT05212 standard; DNA; 27 BP.  
 XX  
 XX AAT05212;  
 AC  
 XX 13-JUN-1996 (first entry)  
 DT  
 XX Hepatitis C virus antisense oligonucleotide A65.  
 DE  
 XX Inhibition; expression; hepatitis C virus; HCV; non-A; non-B; RNA;  
 KW translation; in vivo; ex vivo; in vitro; treatment; prevention;  
 KW infection; antisense; non coding; region; NCR; core region; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX WO9530746-A1.  
 PN  
 XX 16-NOV-1995.  
 PD  
 XX 08-MAY-1995; 95WO-US005812.  
 PF  
 XX 10-MAY-1994; 94US-00240382.  
 PR  
 XX (GEHO) GEN HOSPITAL CORP.  
 PA  
 XX Wakita T, Wands JR;  
 PI  
 XX WPI; 1995-404113/51.  
 DR  
 XX New anti-sense hepatitis C virus oligo:nucleotide(s) - used for  
 PT inhibiting HCV RNA translation, for the treatment or prevention of HCV  
 PT infection.  
 PT  
 XX Claim 1; Page 26; 50pp; English.  
 PS  
 XX The present oligonucleotide (ON) inhibits the expression of hepatitis C  
 CC virus (HCV) RNA, specifically HCV type II and type III protein synthesis  
 CC is inhibited by 74% and 54%, respectively. The ONs of the invention  
 CC inhibit translation of HCV types I-V RNA in vivo, ex vivo or in vitro,  
 CC and can therefore be used to treat or prevent HCV infection. The  
 CC antisense ONs comprise 10-28 nucleotides complementary to the entire HCV  
 CC 5'-non-coding and part of the core region. The A or S in the ONs name

CC denotes antisense or sense, and the no. indicates the position of the 5'-  
CC end of the ON. The ON was tested at 10 fold molar excess to HCV RNA  
XX  
SQ Sequence 27 BP; 8 A; 5 C; 9 G; 5 T; 0 U; 0 Other;

Query Match 98.1%; Score 20.6; DB 2; Length 27;  
Best Local Similarity 95.2%; Pred. No. 3.3;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21  
|||||  
DB 23 CCCTGTGAGGAAGTCTGTCT 3

## RESULT 12

AAH44980  
ID AAH44980 standard; DNA; 27 BP.

XX  
AC AAH44980;

DT 05-SEP-2001 (first entry)

DE HCV specific primer Hcp-98.

XX Multiple viral agent detection; human immunodeficiency virus; HIV;  
KW Hepatitis C virus; HCV; Hepatitis B virus; Hepatitis C virus; HCV;  
KW blood transfusion; blood donation; viral infection; primer; ss.

OS Hepatitis C virus.

XX WO200136442-A1.

PN 25-MAY-2001.

PD 17-NOV-2000; 2000WO-US031738.

PF 17-NOV-1999; 99US-0165916P.

PR (JIJJ/) JI J.

PA (MANA/) MANAK M.

PA (WUKK/) WU K.

PA (CHEN/) CHEN X.

PA (YANG/) YANG L.

XX Ji J, Manak M, Wu K, Chen X, Yang L;

PI WPI; 2001-355605/37.

DR Simultaneous detection of HIV, HBV and HCV in samples useful to test

PT donated blood for viral infection comprises amplification of nucleic

PT acids.

XX Disclosure; Page 16; Slpp; English.

CC This invention relates to a method for detecting multiple viral agents in  
CC a sample. The method consists of amplifying nucleic acids from Human  
CC immunodeficiency virus (HIV), Hepatitis C virus (HCV), and or Hepatitis B  
CC virus (HBV) using a mixture of primers specific for HBV, HCV HIV-1 type M  
CC and HIV-1 type O and detecting their presence. Included in the invention  
CC is a kit for the detection of HIV, HCV, HBV and combinations of them in a  
CC blood or blood product sample. The method can be used to test blood  
CC donated for transfusions for the presence of infection with HIV, HBV or  
CC HCV. The present sequence represents a primer specific for HCV, which can  
CC be used in the method of the invention

XX Sequence 27 BP; 4 A; 9 C; 6 G; 7 T; 0 U; 1 Other;

## Query Match

Best Local Similarity 98.1%; Score 20.6; DB 4; Length 27;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21  
|||||

DB 1 CCCTGTGAGGAAGTCTGTCT 21

## RESULT 13

AAH75858  
ID AAH75858 standard; DNA; 27 BP.

XX  
AC AAH75858;

DT 26-OCT-2001 (first entry)

DE Mycobacterium tuberculosis forward PCR primer p60.

XX PCR primer; ss.

OS Mycobacterium tuberculosis.

XX RU2163638-C1.

PN 27-FEB-2001.

PD 06-DEC-1999; 99RU-00125164.

PF 06-DEC-1999; 99RU-00125164.

PR (ASIB=) AS SIBE BIOCHEM RES INST.

PA Beklemishev AB, Khorosheva EM, Nomokonova N Yu;

PI WPI; 2001-280317/29.

XX Detection of DNA from tuberculosis mycobacterium complex comprising a  
XX polymerase chain reaction method.

PS Claim 9; Col 17-18; 13pp; Russian.

XX The present invention relates to a PCR-based method for the detection of  
CC Mycobacterium tuberculosis. The present sequence is a PCR primer for  
CC Mycobacterium tuberculosis. This sequence was used to illustrate the  
CC method of the present invention

XX Sequence 27 BP; 5 A; 9 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 98.1%; Score 20.6; DB 4; Length 27;

Best Local Similarity 95.2%; Pred. No. 3.3;

Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21

DB 1 CCCTGTGAGGAAGTCTGTCT 21

## RESULT 14

ABN79962  
ID ABN79962 standard; DNA; 27 BP.

XX  
AC ABN79962;

DT 15-JUL-2002 (first entry)

DE Hepatitis C virus PCR primer HCV-PCR-OUTF.

XX Single nucleotide polymorphism; nucleic acid typing; hepatitis C virus;  
XX tissue typing; PCR; primer; HCV; ss.

OS Hepatitis C virus.

XX WO200220837-A2.

XX 14-MAR-2002.

XX 10-SEP-2001; 2001WO-GB004042.

XX

PR 08-SEP-2000; 2000GB-00022069.  
 XX (PYRO-) PYROSEQUENCING PA.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PA (GARD/) GARDNER R.  
 XX  
 PI Ronaghi M, Ekstroem B, Pourmand N;  
 XX WPI; 2002-393849/42.  
 DR  
 XX  
 XX Typing nucleic acid for obtaining information about several variable  
 PT sites involves simultaneously or sequentially performing two or more  
 PT primer extension reactions, and determining the pattern of nucleotide  
 PT incorporation.  
 XX  
 XX Example 1; Page 43; 86pp; English.  
 PS  
 XX The invention relates to a novel method for obtaining typing information  
 CC about several variable sites within target nucleic acid, or typing one or  
 CC more nucleic acid molecules. The methods of the invention are useful for  
 CC typing one or more nucleic acid molecules containing two or more variable  
 CC sites, preferably nucleic acid molecules containing three or more  
 CC variable sites are typed, where three or more primer extension reactions  
 CC are performed. The method is also useful for diagnosis of pathological  
 CC conditions characterized by the presence of specific nucleic acid  
 CC molecule(s). The methods are particularly suited for identifying  
 CC microbial species or their subtypes, and in typing procedures e.g. typing  
 CC of polymorphisms, tissue typing or in clinical applications. The sequence  
 CC represents a PCR primer used in the invention to type hepatitis C virus  
 CC (HCV) positive sera  
 XX  
 XX Sequence 27 BP; 4 A; 9 C; 6 G; 7 T; 0 U; 1 Other;  
 SQ

Query Match 98.1%; Score 20.6; DB 6; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 3.3;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAACTWCTGTCT 21  
 |||||  
 Db 1 CCTGTGAGGAACTWCTGTCT 21  
 |||||

RESULT 15  
 AAT05239  
 ID AAT05239 standard; DNA; 28 BP.  
 AC  
 XX AAT05239;  
 XX  
 DT 13-JUN-1996 (first entry)  
 XX  
 DE Hepatitis C virus sense oligonucleotide S38.  
 XX  
 XX Inhibition; expression; hepatitis C virus; HCV; non-A; non-B; RNA;  
 KW translation; in vivo; ex vivo; in vitro; treatment; prevention;  
 KW infection; sense; non coding; region; NCR; core region; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX WO9530746-A1.  
 PN  
 XX  
 PD 16-NOV-1995.  
 XX  
 XX 08-MAY-1995; 95WO-US005812.  
 PF  
 XX  
 PR 10-MAY-1994; 94US-00240382.  
 XX  
 XX (GEHO ) GEN HOSPITAL CORP.  
 PA  
 XX Wakita T, Wands JR;  
 PI  
 XX WPI; 1995-404113/51.  
 DR  
 XX  
 XX New anti-sense hepatitis C virus oligo:nucleotide(s) - used for

PT inhibiting HCV RNA translation, for the treatment or prevention of HCV  
 PT infection.  
 XX  
 PS Example; Page 33; 50pp; English.  
 XX  
 CC The present oligonucleotide (ON) inhibits the expression of hepatitis C  
 CC virus (HCV) RNA, specifically HCV type II and type III protein synthesis  
 CC is inhibited by -4% and ND, respectively. The ONs of the invention  
 CC inhibit translation of HCV types I-V RNA in vivo, ex vivo or in vitro,  
 CC and can therefore be used to treat or prevent HCV infection. The  
 CC antisense ONs comprise 10-28 nucleotides complementary to the entire HCV  
 CC 5'-non-coding and part of the core region. The A or S in the ONs name  
 CC denotes antisense or sense, and the no. indicates the position of the 5'-  
 CC end of the ON. The ON was tested at 10 fold molar excess to HCV RNA, and  
 CC ND denotes not determined  
 XX  
 XX Sequence 28 BP; 5 A; 10 C; 5 G; 8 T; 0 U; 0 Other;  
 SQ

Query Match 98.1%; Score 20.6; DB 2; Length 28;  
 Best Local Similarity 95.2%; Pred. No. 3.3;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAACTWCTGTCT 21  
 |||||  
 Db 6 CCTGTGAGGAACTACTGTCT 26  
 |||||

RESULT 16  
 AAZ57748/c  
 ID AAZ57748 standard; DNA; 28 BP.  
 XX  
 AC AAZ57748;  
 XX  
 DT 05-APR-2000 (first entry)  
 XX  
 DE Hepatitis C virus antisense inhibitor oligonucleotide A65.  
 XX  
 KW Hepatitis C virus; HCV; antisense oligonucleotide; hepatotropic; ss;  
 KW anti-inflammatory; translation inhibition; HCV infection; virucide.  
 XX  
 OS Hepatitis C virus.  
 XX  
 XX US6001990-A.  
 PN  
 XX  
 PD 14-DEC-1999.  
 XX  
 PF 07-JUN-1995; 95US-00474700.  
 XX  
 PR 10-MAY-1994; 94US-00240382.  
 XX  
 XX (GEHO ) GEN HOSPITAL CORP.  
 PA  
 XX Moradpour D, Wands JR, Wakita T;  
 PI  
 XX WPI; 2000-104900/09.  
 DR  
 XX Antisense oligonucleotide to Hepatitis C virus RNA, useful for treating  
 PT Hepatitis C virus infections.  
 PT  
 PS Claim 3; Col 19; 31pp; English.  
 XX  
 CC This sequence is an antisense oligonucleotide that hybridises to  
 CC Hepatitis C virus (HCV) RNA, under physiological conditions. The  
 CC invention relates to HCV antisense oligonucleotides, and also for a  
 CC vector comprising a nucleotide sequence which is transcribed in an animal  
 CC cell to generate an antisense oligonucleotide. The oligonucleotides have  
 CC virucide, hepatotropic and anti-inflammatory activity, and are useful for  
 CC treating HCV infection by inhibiting translation of type I-V HCV RNA.  
 CC Hepatitis C virus is a positive strand RNA virus, and is the major  
 CC causative agent of post-transfusion hepatitis. Persistent HCV infection  
 CC can lead to chronic hepatitis, cirrhosis, and hepatocellular carcinoma  
 XX  
 XX Sequence 28 BP; 8 A; 5 C; 10 G; 5 T; 0 U; 0 Other;



Query Match 98.1%; Score 20.6; DB 3; Length 28;  
 Best Local Similarity 95.2%; Pred. No. 3.3;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAACCTGCTCT 21  
 |||||:|||||:  
 Db 23 CCCTGTGAGGAACCTGCTCT 3

RESULT 17  
 AAZ57779  
 ID AAZ57779 standard; DNA; 28 BP.  
 XX  
 AC AAZ57779;  
 DT  
 XX 05-APR-2000 (first entry)  
 XX Hepatitis C virus sense oligonucleotide S38.  
 DE  
 XX Hepatitis C virus; HCV; sense oligonucleotide; ss;  
 KW anti-inflammatory; translation inhibition; HCV infection; virucide.  
 XX  
 OS Hepatitis C virus.  
 XX  
 XX US6001990-A.  
 PN  
 XX  
 XX 14-DEC-1999.  
 PD  
 XX 07-JUN-1995; 95US-00474700.  
 PF  
 XX 10-MAY-1994; 94US-00240382.  
 PR  
 XX (GEHO ) GEN HOSPITAL CORP.  
 PA  
 XX Moradpour D, Wands JR, Wakita T;  
 PI  
 XX WPI; 2000-104900/09.  
 DR  
 XX Antisense oligonucleotide to Hepatitis C virus RNA, useful for treating  
 PT Hepatitis C virus infections.  
 PT  
 PS Disclosure; Col 27; 3lpp; English.  
 XX  
 CC This sequence is an sense oligonucleotide used in the method of the  
 CC invention. The invention relates to hepatitis C virus (HCV) antisense  
 CC oligonucleotides that hybridise to HCV RNA under physiological  
 CC conditions. The also relates to a vector comprising a nucleotide sequence  
 CC which is transcribed in an animal cell to generate an antisense  
 CC oligonucleotide. The oligonucleotides have virucide, hepatotropic and  
 CC anti-inflammatory activity, and are useful for treating HCV infection by  
 CC inhibiting translation of type I-V HCV RNA. Hepatitis C virus is a  
 CC positive strand RNA virus, and is the major causative agent of post-  
 CC transfusion hepatitis. Persistent HCV infection can lead to chronic  
 CC hepatitis, cirrhosis, and hepatocellular carcinoma  
 XX  
 SQ Sequence 28 BP; 5 A; 10 C; 5 G; 8 T; 0 U; 0 Other;

Query Match 98.1%; Score 20.6; DB 3; Length 28;  
 Best Local Similarity 95.2%; Pred. No. 3.3;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAACCTGCTCT 21  
 |||||:|||||:  
 Db 6 CCCTGTGAGGAACCTGCTCT 26

RESULT 18  
 ADV04753  
 ID ADV04753 standard; DNA; 28 BP.  
 XX  
 AC ADV04753;  
 XX

DT 24-FEB-2005 (first entry)  
 XX  
 DE Synthetic PCR primer #4.  
 XX  
 KW Virucide; hepatitis C virus infection; ss; replicon; PCR; primer.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2004104198-A1.  
 XX  
 PD 02-DEC-2004.  
 XX  
 XX 25-NOV-2003; 2003WO-JP015038.  
 PF  
 XX 26-MAY-2003; 2003JP-00148242.  
 PR  
 XX 19-SEP-2003; 2003JP-00329115.  
 PR  
 XX (TORA ) TORAY IND INC.  
 PA (TOKM-) TOKYO METROPOLITAN ORG MEDICAL RES.  
 PA (UYMA-) UNIV MAINZ GUTENBERG JOHANNES.  
 XX  
 XX Wakita T, Kato T, Date T;  
 PI  
 XX WPI; 2005-013292/01.  
 DR  
 XX Novel replicon RNA, having sequence of 5' and 3' untranslated region and  
 PT base sequence encoding NS3, NS4A, NS4B, NS5A and NS5B proteins on genomic  
 PT RNA of hepatitis C virus of genotype 2a, useful for treating hepatitis C  
 PT virus infection.  
 XX  
 PS Example 5; SEQ ID NO 19; 197pp; Japanese.  
 XX  
 CC The invention relates to replicon RNA from genotype 2a of hepatitis C  
 CC virus comprising a 5' untranslated region, a base sequence encoding NS3  
 CC protein, NS4A protein, NS4B protein, NS5A protein and NS5B protein, and a  
 CC 3' untranslated region. The invention also relates to a cell capable of  
 CC reproducing the replicon involving transducing the replicon RNA to a  
 CC cell, a method of producing a hepatitis C virus protein, a method of  
 CC screening a substance that promotes or suppresses the reproduction of  
 CC hepatitis C virus, involving culturing the replicon reproducing cell in  
 CC the presence of a test substance, and detecting the reproduction of  
 CC replicon RNA in the culture. Virucide. The replicon RNA is useful for  
 CC producing a replicon reproduction cell and for increasing the  
 CC reproduction efficiency of replicon RNA of hepatitis C virus of genotype  
 CC 2a. The cell and the replicon RNA are useful for producing a therapeutic  
 CC agent or a diagnostic agent for hepatitis C virus infection, for  
 CC producing a vaccine against hepatitis C virus infection, and for screening  
 CC a substance that promotes or suppresses the reproduction of hepatitis C  
 CC virus. This sequence represents a PCR primer used in the scope of the  
 CC invention.  
 XX  
 SQ Sequence 28 BP; 5 A; 10 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 98.1%; Score 20.6; DB 14; Length 28;  
 Best Local Similarity 95.2%; Pred. No. 3.3;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAACCTGCTCT 21  
 |||||:|||||:  
 Db 2 CCCTGTGAGGAACCTGCTCT 22

RESULT 19  
 ADV04766  
 ID ADV04766 standard; DNA; 28 BP.  
 XX  
 AC ADV04766;  
 XX  
 XX 24-FEB-2005 (first entry)  
 DT  
 XX Synthetic PCR primer #17.  
 DE  
 XX Virucide; hepatitis C virus infection; ss; replicon; PCR; primer.  
 KW

```
XX OS Synthetic.
XX FH WO2004104198-A1.
XX PN
XX XX
XX PD 02-DEC-2004.
XX XX
XX PF 25-NOV-2003; 2003WO-JP015038.
XX XX
XX PR 26-MAY-2003; 2003JP-00148242.
XX PR 19-SEP-2003; 2003JP-00329115.
XX XX
XX PA (TORA ) TORAY IND INC.
XX PA (TOKM-) TOKYO METROPOLITAN ORG MEDICAL RES.
XX PA (UYMA-) UNIV MAINZ GUTENBERG JOHANNES.
XX PI Wakita T, Kato T, Date T;
XX XX
XX DR WPI; 2005-013292/01.
XX XX
XX PT Novel replicon RNA, having sequence of 5' and 3' untranslated region and
XX PT base sequence encoding NS3, NS4A, NS4B, NS5A and NS5B proteins on genomic
XX PT RNA of hepatitis C virus of genotype 2a, useful for treating hepatitis C
XX PT virus infection.
XX XX
XX PS Example 7; SEQ ID NO 32; 197pp; Japanese.
XX XX
XX CC The invention relates to replicon RNA from genotype 2a of hepatitis C
XX CC virus comprising a 5' untranslated region, a base sequence encoding NS3
XX CC protein, NS4A protein, NS4B protein, NS5A protein and NS5B protein, and a
XX CC 3' untranslated region. The invention also relates to a cell capable of
XX CC reproducing the replicon involving transducing the replicon RNA to a
XX CC cell, a method of producing a hepatitis C virus protein, a method of
XX CC screening a substance that promotes or suppresses the reproduction of
XX CC hepatitis C virus, involving culturing the replicon reproducing cell in
XX CC the presence of a test substance, and detecting the reproduction of
XX CC replicon RNA in the culture. Virucide. The replicon RNA is useful for
XX CC producing a replicon reproduction cell and for increasing the
XX CC reproduction efficiency of replicon RNA of hepatitis C virus of genotype
XX CC 2a. The cell and the replicon RNA are useful for producing a therapeutic
XX CC agent or a diagnostic agent for hepatitis C virus infection, for screening
XX CC producing a vaccine against hepatitis C virus infection and for screening
XX CC a substance that promotes or suppresses the reproduction of hepatitis C
XX CC virus. This sequence represents a PCR primer used in the scope of the
XX CC invention.
XX SQ Sequence 28 BP; 5 A; 10 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 98.1%; Score 20.6; DB 14; Length 28;
Best Local Similarity 95.2%; Pred. No. 3.3;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAACACTWCTGTCT 21
Db 2 CCCTGTGAGGAACACTGTCT 22

RESULT 20
AAAT09176/c
ID AAAT09176 standard; DNA; 45 BP.
XX AC
XX AC AAAT09176;
XX XX
XX DT 21-OCT-2004 (revised)
XX DT 14-AUG-1996 (first entry)
XX XX
XX DE Hepatitis C virus specific capture/amp-probe-1 (HCV A).
XX XX
XX KW Ligase dependent polymerase chain reaction; LD-PCR; probe; hybridisation;
XX KW ligand binding pair; ligase; paramagnetic bead; primer; amplification;
XX KW hepatitis; untranslated region; UTR; rRNA; ss.
XX OS Synthetic.
```

```
XX FH Key misc_binding Location/Qualifiers
XX FT 5...45
XX FT /*tag= a
XX FT /bound moiety
XX FT /note="complementary to Hepatitis C virus 5'
XX FT untranslated region"
XX XX
XX PN W09535390-A1.
XX XX
XX PD 28-DEC-1995.
XX XX
XX PF 14-JUN-1995; 95WO-US007671.
XX XX
XX PR 22-JUN-1994; 94US-00263937.
XX XX
XX PA (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX XX
XX PI Zhang DY;
XX XX
XX DR WPI; 1996-058427/06.
XX XX
XX PT Ligase dependent polymerase chain reaction - for the detection of
XX PT infectious pathogens and abnormal human genes, e.g. HIV and neoplasia.
XX XX
XX PS Claim 47; Page 52; 100pp; English.
XX XX
XX CC A novel method of detecting a target nucleic acid (TNA) sequence involves
XX CC use of the ligase dependent polymerase chain reaction method (LD-PCR). In
XX CC this method, two probes are provided. The first probe contains a region
XX CC at the 5' end which is complementary and will hybridise with the TNA, the
XX CC 3' end of the first probe is generic and is bound to one half of a ligand
XX CC binding pair (LBP). The second probe contains a region at the 5' end
XX CC which is complementary to a region in the TNA which is immediately
XX CC adjacent to the complementary region of the first probe. When the probes
XX CC are bound to the TNA, they can be ligated together using a conventional
XX CC ligase. The TNA-ligated probe complex can be isolated by binding the
XX CC first probe to a paramagnetic bead to which is attached the second half
XX CC of the LBP. The TNA can be dissociated from the ligated probe complex
XX CC which can then be detected either by a label attached to the second
XX CC probe, by using an external probe or by PCR using the ligated probes as a
XX CC template. The capture probes AA09176-7 are used to isolated a region of
XX CC the Hepatitis C virus 5' untranslated region. This region can then be
XX CC detected by the probes AA09178-9 to produce the ligated amplification
XX CC sequence AA09180. The ligated sequence can subsequently be detected by
XX CC PCR amplification with the primers AA09181-3
XX CC
XX CC Revised record issued on 21-OCT-2004 : Correction to Feature Table Key
XX SQ Sequence 45 BP; 13 A; 7 C; 15 G; 10 T; 0 U; 0 Other;

Query Match 98.1%; Score 20.6; DB 2; Length 45;
Best Local Similarity 95.2%; Pred. No. 3.5;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAACACTWCTGTCT 21
Db 31 CCCTGTGAGGAACACTGTCT 11

RESULT 21
AAV20717/c
ID AAV20717 standard; DNA; 45 BP.
XX AC
XX AC AAV20717;
XX XX
XX DT 17-JUL-1998 (first entry)
XX XX
XX DE Hepatitis C virus probe SEQ ID NO:22.
XX KW Hepatitis C virus; HCV; HIV; probe; detection; capture; amplification;
XX KW paramagnetic particle; ligation; ss.
XX XX
```

OS Synthetic.  
 OS Hepatitis C virus.  
 PN WO9804745-A1.  
 XX  
 XX  
 PD  
 XX 05-FEB-1998.  
 XX  
 PF 30-JUL-1997; 97WO-US013390.  
 XX  
 PR 31-JUL-1996; 96US-00690495.  
 XX  
 XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.  
 PA  
 XX Zhang DY, Brandwein M;  
 PI WPI; 1998-159153/14.  
 DR  
 XX  
 XX  
 XX  
 PT Detection of target nucleic acids in samples - using capture and  
 PT amplification probes, paramagnetic particles and ligation to form a  
 PT nucleotide sequence which can be detected.  
 XX  
 PS Example 4; Page 62; 136pp; English.  
 XX  
 CC The present sequence represents a probe used in an example of the present  
 CC invention for the detection of HCV RNA in a sample. The present invention  
 CC describes methods for: (A) detecting a target nucleic acid (NA) in a  
 CC sample; (B) in situ detection of a target NA in a sample; (C) detecting  
 CC an antigen in a sample; and (D) detecting an antibody in a sample. The  
 CC methods can be used for the rapid automated detection and monitoring of  
 CC pathogenic organisms, as well as the detection of abnormal genes in an  
 CC individual. The methods allow for isolation, amplification and detection  
 CC of NA sequences corresponding to the target NA to be carried out in the  
 CC same receptacle, e.g. tube or micro-well plate. The method also allows  
 CC for standardisation of conditions, because only a pair of generic  
 CC amplification probes may be utilised in the present method for detecting  
 CC a variety of target NAs, thus allowing efficient multiplex amplification.  
 CC The method also allows the direct detection of RNA by probe amplification  
 CC without the need for DNA template production. The amplification probes,  
 CC which may be covalently joined end to end, form a contiguous ligated  
 CC amplification sequence. The assembly of the amplifiable DNA by ligation  
 CC increase specificity, and makes possible the detection of a single  
 CC mutation in a target  
 XX  
 SQ Sequence 45 BP; 13 A; 7 C; 15 G; 10 T; 0 U; 0 Other;  
 Query Match 98.1%; Score 20.6; DB 2; Length 45;  
 Best Local Similarity 95.2%; Pred. No. 3.5;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CCCTGTGAGGAAGTCTGTCT 21  
 DB 31 CCCTGTGAGGAAGTCTGTCT 11  
 RESULT 22  
 AAV05026/c  
 ID AAV05026 standard; DNA; 45 BP.  
 XX  
 XX  
 AC AAV05026;  
 XX  
 DT 25-JUN-1998 (first entry)  
 XX  
 DE Probe PA of the specification.  
 XX  
 XX Human immunodeficiency virus type 1; separation; microbe; PCR primer;  
 KW amplify; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP10001493-A.  
 XX  
 PD 06-JAN-1998.  
 XX

PF 24-FEB-1997; 97JP-00039135.  
 XX  
 PR 26-FEB-1996; 96EP-00102812.  
 XX  
 PA (JAPS ) NIPPON GOSEI GOMU KK.  
 XX  
 DR WPI; 1998-114803/11.  
 XX  
 PT Separation of nucleic acids from sample - comprises isolation of  
 PT microbial genetic material, probing and recovering target molecule.  
 XX  
 PS Disclosure; Page 8; 12pp; Japanese.  
 XX  
 CC PCR primers AAV05022-25. appear in the specification. They are used to  
 CC amplify part of the Human immunodeficiency virus type I nucleic acid. The  
 CC specification describes a method for the separation of a target microbial  
 CC nucleic acid from a biological fluid sample. The method comprises  
 CC isolating a liquid fraction comprising a microorganism from a sample,  
 CC isolating the microbial nucleic acid from the liquid fraction, combining  
 CC a probe with the nucleic acid and recovering the probed nucleic acid. A  
 CC protein denaturing agent is added between any of the steps  
 XX  
 SQ Sequence 45 BP; 10 A; 16 C; 11 G; 8 T; 0 U; 0 Other;  
 Query Match 98.1%; Score 20.6; DB 2; Length 45;  
 Best Local Similarity 95.2%; Pred. No. 3.5;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CCCTGTGAGGAAGTCTGTCT 21  
 DB 25 CCCTGTGAGGAAGTCTGTCT 5  
 RESULT 23  
 AAV22769/c  
 ID AAV22769 standard; DNA; 45 BP.  
 XX  
 AC AAV22769;  
 XX  
 DT 27-AUG-2003 (revised)  
 DT 22-JUL-1998 (first entry)  
 XX  
 DE Capture/Amp-probe-1 (HCV A) for detecting Hepatitis C virus 5' UTR RNA.  
 XX  
 KW Probe; Capture/Amp-probe-1 (HCV A); automated detection; Mycobacteri-  
 KW nucleic acid; monitoring; pathogenic organism; abnormal gene; ss.  
 XX  
 OS Synthetic.  
 OS Hepatitis C virus.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1  
 FT /tag= a  
 FT /note= "Biotinylated"  
 XX  
 PN WO9804746-A1.  
 XX  
 PD 05-FEB-1998.  
 XX  
 PF 30-JUL-1997; 97WO-US013391.  
 XX  
 PR 31-JUL-1996; 96US-00690494.  
 XX  
 PA (MOUN ) MOUNT SINAI SCHOOL MEDICINE.  
 XX  
 PI Zhang DY, Brandwein M, Heuh TCH;  
 XX  
 DR WPI; 1998-159154/14.  
 XX  
 PT Detection of target nucleic acids in samples - using capture and  
 PT amplification probes, paramagnetic particles and ligation to form a  
 PT nucleotide sequence which is amplified.  
 XX



PT Detecting target nucleic acids in a sample by analyzing differential mRNA  
PT expression, useful for carrying out clinical assays for the detection of  
PT infectious pathogenic agents or microorganisms and abnormal genes in an  
PT individual.

XX Example 5; Page 78; 166pp; English.

XX The invention relates to methods and kits for rapid automated detection  
CC of infectious pathogenic agents and normal and abnormal genes. It also  
CC relates to a method for detecting target nucleic acids in a sample by  
CC analysing differential mRNA expression. The methods and compositions are  
CC useful for carrying out clinical assays for the rapid, automated  
CC detection of infectious pathogenic agents or microorganisms, as well as  
CC to detect abnormal genes, like in tumour conditions, in an individual.  
CC The present sequence is a probe used to detect Hepatitis C virus (HCV)  
CC RNA. This sequence is used to illustrate the method of the invention

XX Sequence 45 BP; 13 A; 7 C; 15 G; 10 T; 0 U; 0 Other;

Query Match 98.1%; Score 20.6; DB 8; Length 45;

Best Local Similarity 95.2%; Pred. NO. 3.5;

Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCCTGTGAGGAAGTCTGTCT 21

DB 31 CCCTGTGAGGAAGTCTGTCT 11

RESULT 26

ADQ74915/c

ID ADQ74915 standard; DNA; 45 BP.

AC ADQ74915;

DT 07-OCT-2004 (first entry)

DE HCV Capture/Amp probe 1 (HCV-A).

XX Ligation dependent PCR; LD PCR; ss; probe; capture/amplification probe;  
KW polymerase chain reaction; strand displacement amplification;  
KW transcription mediated amplification;  
KW ramification-extension amplification method; RAM; primer extension;  
KW differential mRNA expression; genetic variation; genetic disease;  
KW neoplasm; infectious agent; HCV.

XX Hepatitis C virus.

OS Synthetic.

XX US2004137484-A1.

PD 15-JUL-2004.

PF 21-NOV-2003; 2003US-00719480.

XX 15-OCT-2001; 2001US-00978261.

PR 15-OCT-2002; 2002WO-US032745.

PA (ZHAN/) ZHANG D Y.

PA (ZHAN/) ZHANG W.

PA (YIJU/) YI J.

PI Zhang DY, Zhang W, Yi J;

XX WPI; 2004-533357/51.

XX Detecting target nucleic acid in sample, by contacting target nucleic  
PT acid with circular oligonucleotide probe, adding specific primer pairs,  
PT signal moiety, DNA polymerase, and amplifying circular oligonucleotide  
PT probe.

XX Example 5; SEQ ID NO 22; 77pp; English.

CC The invention relates to detecting (M1) a target nucleic acid in a

CC sample, involving contacting the target nucleic acid with a circular  
CC oligonucleotide probe under conditions that allow hybridisation between  
CC complementary sequences in the target nucleic acid and the circular  
CC oligonucleotide probe, adding at least one forward primer comprising a  
CC sequence complementary to a portion of the circular oligonucleotide  
CC probe, adding an oligonucleotide primer pair comprising a first primer  
CC and a second primer where the first primer of the pair comprises a first  
CC sequence that is substantially identical to a portion of the circular  
CC oligonucleotide probe, a second sequence that is complementary to the  
CC second primer of the pair, and a signal generating moiety, the second  
CC primer of the pair comprises a sequence that is complementary to the  
CC first primer and a moiety capable of quenching, masking or inhibiting the  
CC activity of the signal generating moiety, and when the first primer and  
CC the second primer are bound to one another, the signal is inhibited,  
CC adding at least one reverse primer comprising a sequence that is  
CC substantially identical to a portion of the circular oligonucleotide  
CC probe, adding a DNA polymerase, and amplifying the circular  
CC oligonucleotide probe and separating the signal generating moiety and the  
CC quenching, masking or inhibitory moiety to generate a signal, where  
CC detection of signal indicates the presence of the target nucleic acid in  
CC the sample. Also included are a kit for (M1), and amplifying (M2) a  
CC circular nucleic acid sequence. In (M1), the circular oligonucleotide  
CC probe is formed by ligating the 3' and 5' ends of linear oligonucleotide  
CC probe, comprising 3' and 5' ends regions complementary to adjacent  
CC sequences in the target nucleic acid under conditions that allow  
CC hybridisation between complementary sequences in the target nucleic acid  
CC and the linear oligonucleotide probe. The circular probe is amplified  
CC using an amplification method chosen from polymerase chain reaction,  
CC strand displacement amplification, transcription mediated amplification,  
CC ramification-extension amplification method (RAM) and primer extension.  
CC (M1) is useful for detecting a target nucleic acid in a sample. (M2) is  
CC useful for amplification of genomic DNA and total mRNAs expressed in  
CC cells and for analysing differential mRNA expression. (M1) is useful for  
CC detecting genetic variations in nucleic acids in sample from patients  
CC with genetic diseases or neoplasia. The DNA and/or mRNA amplified by (M2)  
CC is used in techniques developed for detection of infectious agents, and  
CC detection of normal and abnormal genes. (M1) is used in clinical assays  
CC to detect and monitor pathogenic microorganisms in a test sample, as well  
CC as to detect abnormal genes in an individual. (M1) is useful for routine  
CC diagnostic testing in a clinical laboratory setting. The present sequence  
CC is a capture/amplification probe used to demonstrate the above methods.

XX Sequence 45 BP; 13 A; 7 C; 15 G; 10 T; 0 U; 0 Other;

Query Match 98.1%; Score 20.6; DB 12; Length 45;

Best Local Similarity 95.2%; Pred. No. 3.5;

Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCCTGTGAGGAAGTCTGTCT 21

DB 31 CCCTGTGAGGAAGTCTGTCT 11

RESULT 27

AEB17467/c

ID AEB17467 standard; DNA; 45 BP.

AC AEB17467;

XX 08-SEP-2005 (first entry)

DT HCV 5'UTR RNA probe, Capture/Amp-probe-1 (HCV A) SEQ ID No:22.

DE DNA detection; RNA detection; hybridization; 5'UTR; probe; ss.

XX Hepatitis C virus.

OS Synthetic.

XX WO2005061722-A1.

XX 07-JUL-2005.

XX 21-NOV-2003; 2003WO-US037199.

XX PR 21-NOV-2003; 2003WO-US037199.  
XX PA (MOUN ) MOUNT SINAI SCHOOL MEDICINE.  
XX PA (ZHAN/) ZHANG D Y.  
XX PA (ZHAN/) ZHANG W.  
XX PA (YIUJ/) YI J.  
XX PI Zhang DY, Zhang W, Yi J;  
XX PI WPI; 2005-488654/49.  
XX PT Detecting target nucleic acid for detecting pathogenic agents, by  
XX PT contacting target nucleic acid with circular oligonucleotide probe and  
XX PT amplifying circular oligonucleotide probe to generate signal, indicating  
XX PT presence of nucleic acid.  
XX PS Example 5; SEQ ID NO 22; 145pp; English.  
XX SS The invention relates to a method of detecting a target nucleic acid in a  
XX CC sample. The method comprises: (a) contacting the target nucleic acid with  
XX CC a circular oligonucleotide probe that allows hybridization between  
XX CC complementary sequences in the target nucleic acid and the circular  
XX CC oligonucleotide probe; (b) adding at least one forward primer comprising  
XX CC a sequence complementary to a portion of the circular oligonucleotide  
XX CC probe; (c) adding an oligonucleotide primer pair comprising a first  
XX CC primer and a second primer, where the first primer of the pair comprises  
XX CC a first sequence that is substantially identical to a portion of the  
XX CC circular oligonucleotide probe, a second sequence that is complementary  
XX CC to the second primer of the pair, and a signal generating moiety; the  
XX CC second primer of the pair comprises a sequence that is complementary to  
XX CC the first primer and a moiety capable of quenching, masking, or  
XX CC inhibiting the activity of the signal generating moiety when located  
XX CC adjacent to, or in close proximity to, the signal generating moiety; and  
XX CC when the first primer and the second primer are bound to one another, the  
XX CC signal is inhibited; (d) adding at least one reverse primer comprising a  
XX CC sequence that is substantially identical to a portion of the circular  
XX CC oligonucleotide probe; (e) adding a DNA polymerase; and (f) amplifying  
XX CC the circular oligonucleotide probe thus separating the signal generating  
XX CC moiety and the quenching, masking, or inhibitory moiety to generate a  
XX CC signal, where detection indicates the presence of the target nucleic acid  
XX CC in the sample. Also described are various kits for detecting a target  
XX CC nucleic acid. The method and kits of the invention are useful for  
XX CC detecting a target nucleic acid in a sample. They are also useful for the  
XX CC detection of pathogenic agents, and normal and abnormal genes. This  
XX CC sequence represents a probe for the 5'UTR region of Hepatitis C virus  
XX CC (HCV) RNA.  
XX SQ Sequence 45 BP; 13 A; 7 C; 15 G; 10 T; 0 U; 0 Other;  
Query Match 98.1%; Score 20.6; DB 14; Length 45;  
Best Local Similarity 95.2%; Pred. No. 3.5;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CCTGTGAGGAAGTCTGTCT 21  
Db 31 CCTGTGAGGAAGTCTGTCT 11  
RESULT 28  
AEB54511/c  
ID AEB54511 standard; DNA; 45 BP.  
XX AC AEB54511;  
XX AC AEB54511;  
XX DT 22-SEP-2005 (first entry)  
XX DE HCV detecting probe Capture/Amp-probe-1 SEQ ID NO 22.  
XX DE ss; probe; DNA detection; screening.  
XX KW Hepatitis C virus.  
XX OS  
XX FT

PN WO2005060725-A2.  
XX PD 07-JUL-2005.  
XX XX 10-MAR-2004; 2004WO-US007237.  
XX PF 21-NOV-2003; 2003US-00791480.  
XX PR (MOUN ) MOUNT SINAI SCHOOL MEDICINE.  
XX PA (ZHAN/) ZHANG D Y.  
XX PA (ZHAN/) ZHANG W.  
XX PA (YIUJ/) YI J.  
XX PI Zhang DY, Zhang W, Yi J;  
XX PI WPI; 2005-554597/56.  
XX PT Detecting target nucleic acid, by contacting target with specific  
XX PT circular probe, forward primer having sequence complementary to probe,  
XX PT primer pair, reverse primer having sequence identity to probe and  
XX PT polymerase, and amplifying probe.  
XX PS Example 5; SEQ ID NO 22; 171pp; English.  
XX SS This invention describes a novel method of detecting target nucleic acid  
XX CC comprising contacting the target with circular oligonucleotide probe,  
XX CC adding forward primer having sequence complementary to the probe, adding  
XX CC oligonucleotide primer pair, where when the first and second primers are  
XX CC bound to one another, the signal is inhibited, adding reverse primer  
XX CC having sequence identical to portion of the probe, adding a DNA  
XX CC polymerase and amplifying the probe. The detection methods of the  
XX CC invention are useful for 1) amplifying and detecting genomic DNA and  
XX CC total mRNAs and for analyzing differential mRNA expression within  
XX CC different cells; 2) for screening a large number of tumor cells at  
XX CC different stages of tumorigenesis and identification of important genes  
XX CC that are closely related to tumorigenesis; 3) for detecting and  
XX CC quantifying nucleic acids from infectious pathogenic agents, and normal  
XX CC and abnormal genes; 4) for generating increased quantities of DNA and/or  
XX CC mRNA from small number of cells; 5) for rapid, highly sensitive, accurate  
XX CC and automated detection of infectious pathogenic agents and normal and  
XX CC abnormal genes. This sequence represents a probe used to detect Hepatitis  
XX CC C virus infection.  
XX SQ Sequence 45 BP; 13 A; 7 C; 15 G; 10 T; 0 U; 0 Other;  
Query Match 98.1%; Score 20.6; DB 14; Length 45;  
Best Local Similarity 95.2%; Pred. No. 3.5;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CCTGTGAGGAAGTCTGTCT 21  
Db 31 CCTGTGAGGAAGTCTGTCT 11  
RESULT 29  
AAQ53262  
ID AAQ53262 standard; RNA; 51 BP.  
XX AC AAQ53262;  
XX AC AAQ53262;  
XX DT 25-MAR-2003 (revised)  
XX DT 13-JUN-1994 (first entry)  
XX XX Hepatitis C virus probe complex.  
XX DE Detection; HCV; 6:2 probe design.  
XX KW Hepatitis C virus.  
XX OS  
XX FT Key modified\_base 1 Location/Qualifiers  
XX FT /\*tag= a  
XX FT /note= "fluorescein labelled"

```
FT modified_base 51
FT FT /*tag= b
FT /note= "Biotin labelled"
XX
XX WO9324656-A1.
XX
XX 09-DEC-1993.
XX
XX PD
XX
XX PF 24-MAY-1993; 93WO-US0004863.
XX
XX PR 29-MAY-1992; 92US-00891543.
XX
XX PA (ABBO ) ABBOTT LAB.
XX
XX PI Marshall RL, Carrino JJ, Sustachek JC;
XX
XX DR WPI; 1993-405844/50.
XX
XX PT Amplifying known RNA target for use in diagnosis of HIV and HCV infection
XX - by treating sample RNA with oligo-nucleotide probe, extending probe by
XX reverse transcription of target, dissociating probe from target,
XX hybridising 2nd probe with 1st, etc.
XX
XX PS Example 2; Page 16; 49pp; English.
XX
XX CC The sequence is that of a complex formed by probes (AAQ53237-Q53240) used
XX in the detection of hepatitis C virus (HCV) using a 6:2 probe design.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX SQ Sequence 51 BP; 14 A; 16 C; 10 G; 11 T; 0 U; 0 Other;

Query Match 98.1%; Score 20.6; DB 2; Length 51;
Best Local Similarity 95.2%; Pred. No. 3.6;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
Db 16 CCTGTGAGGAAGTCTGTCT 36

RESULT 30
AAZ57776/C
ID AAZ57776 standard; DNA; 67 BP.
XX
XX AC
XX
XX AAZ57776;
XX
XX DT 05-APR-2000 (first entry)
XX
XX DE Hepatitis C virus antisense inhibitor oligonucleotide #42.
XX
XX KW Hepatitis C virus; HCV; antisense oligonucleotide; hepatotropic; ss;
XX anti-inflammatory; translation inhibition; HCV infection; virucide.
XX
XX OS Hepatitis C virus.
XX
XX PN US6001990-A.
XX
XX PD 14-DEC-1999.
XX
XX PF 07-JUN-1995; 95US-00474700.
XX
XX PR 10-MAY-1994; 94US-00240382.
XX
XX PA (GEHO ) GEN HOSPITAL CORP.
XX
XX PI Moradpour D, Wands JR, Wakita T;
XX
XX DR WPI; 2000-104900/09.
XX
XX PT Antisense oligonucleotide to Hepatitis C virus RNA, useful for treating
XX Hepatitis C virus infections.
XX
XX PS Claim 31; Col 33; 31pp; English.
```

```
XX This sequence is an antisense oligonucleotide that hybridises to
CC Hepatitis C virus (HCV) RNA, under physiological conditions. The
CC invention relates to HCV antisense oligonucleotides, and also for a
CC vector comprising a nucleotide sequence which is transcribed in an animal
CC cell to generate an antisense oligonucleotide. The oligonucleotides have
CC virucide, hepatotropic and anti-inflammatory activity, and are useful for
CC treating HCV infection by inhibiting translation of type I-V HCV RNA.
CC Hepatitis C virus is a positive strand RNA virus, and is the major
CC causative agent of post-transfusion hepatitis. Persistent HCV infection
CC can lead to chronic hepatitis, cirrhosis, and hepatocellular carcinoma
XX
XX SQ Sequence 67 BP; 13 A; 15 C; 25 G; 14 T; 0 U; 0 Other;

Query Match 98.1%; Score 20.6; DB 3; Length 67;
Best Local Similarity 95.2%; Pred. No. 3.7;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
Db 25 CCTGTGAGGAAGTCTGTCT 5

RESULT 31
ADW39164
ID ADW39164 standard; RNA; 70 BP.
XX
XX AC ADW39164;
XX
XX DT 24-MAR-2005 (first entry)
XX
XX DE Novel nucleic acid amplification method-related oligonucleotide SeqID1.
XX
XX KW DNA detection; RNA detection; ss.
XX
XX OS Unidentified.
XX
XX PN CN1460722-A.
XX
XX PD 10-DEC-2003.
XX
XX PF 19-MAY-2003; 2003CN-00123596.
XX
XX PR 19-MAY-2003; 2003CN-00123596.
XX
XX PA (TIAN/) TIAN J.
XX
XX PI Tian J, Gong Q;
XX
XX DR WPI; 2004-181274/18.
XX
XX PT Method for nucleic acid amplification detection, comprises using a line
XX probe and a ring probe and a one-step constant temperature reaction.
XX
XX PS Example 1; SEQ ID NO 1; 31pp; Chinese.
XX
XX CC This invention relates to a novel nucleic acid amplification detection
XX method. The invention can implement several operations of nucleic acid
XX hybridization, amplification and detection in the same reaction tube, by
XX only using one kind of DNA polymerase and by means of a one-step constant
XX temperature reaction. The invention is applicable to detection of RNA and
XX DNA. The present sequence is that of an oligonucleotide which was used in
XX the exemplification of the method of the invention.
XX
XX SQ Sequence 70 BP; 17 A; 21 C; 16 G; 0 T; 16 U; 0 Other;

Query Match 98.1%; Score 20.6; DB 13; Length 70;
Best Local Similarity 66.7%; Pred. No. 3.7;
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
Db 18 CCCUGAGGAACUACUGUCU 38
```

RESULT 32  
 AAL40115  
 ID AAL40115 standard; DNA; 73 BP.  
 XX  
 AC AAL40115;  
 XX  
 DT 13-SEP-2002 (first entry)  
 XX  
 DE Pathogenic microorganism detecting PCR primer SEQ ID No 41.  
 XX  
 XX Tuberculosis; Mycobacterium; bovis; BCG; africanum; microti; canotti;  
 KW monitoring therapy; pathogenic microorganism; PCR; primer; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200252043-A1.  
 XX  
 PD 04-JUL-2002.  
 XX  
 PF 26-DEC-2001; 2001WO-JP011422.  
 XX  
 PR 26-DEC-2000; 2000JP-00396222.  
 XX  
 PR 26-DEC-2000; 2000JP-00396321.  
 XX  
 PR 29-JUN-2001; 2001JP-00199552.  
 XX  
 PR 13-SEP-2001; 2001JP-00278920.  
 XX  
 PA (TAKI ) TAKARA SHUZO CO LTD.  
 XX  
 PI Shimada M, Hino F, Kato I;  
 XX  
 DR WPI; 2002-500769/53.  
 XX  
 XX Detecting pathogenic microorganisms with oligonucleotide probes and  
 PT primers, useful in disease diagnosis and monitoring therapy.  
 XX  
 PS Claim 57; Page 97; 106pp; Japanese.  
 XX  
 CC The invention relates to a probe containing a 410 or 20 base pair  
 CC sequence, given in the specification. It is capable of detecting the  
 CC tuberculosis bacterial group including Mycobacterium tuberculosis,  
 CC Mycobacterium bovis BCG, Mycobacterium africanum, Mycobacterium microti  
 CC and/or Mycobacterium canotti. The method is useful in disease diagnosis  
 CC and monitoring therapy. This polynucleotide sequence represents a PCR  
 CC primer relating to the detection of pathogenic microorganisms of the  
 CC invention  
 XX  
 SQ Sequence 73 BP; 18 A; 23 C; 15 G; 17 T; 0 U; 0 Other;  
 Query Match 98.1%; Score 20.6; DB 6; Length 73;  
 Best Local Similarity 95.2%; Pred. No. 3.7;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CCCTGTGAGGAAGTCTGTCT 21  
 DB 21 CCCTGTGAGGAAGTCTGTCT 41  
 RESULT 33  
 ADW39166/c  
 ID ADW39166 standard; DNA; 79 BP.  
 XX  
 AC ADW39166;  
 XX  
 DT 24-MAR-2005 (first entry)  
 XX  
 DE Novel nucleic acid amplification method-related oligonucleotide SeqID3.  
 XX  
 DE DNA detection; RNA detection; ss.  
 KW  
 XX Unidentified.  
 OS  
 XX

PN CN1460722-A.  
 XX  
 PD 10-DEC-2003.  
 XX  
 PF 19-MAY-2003; 2003CN-00123596.  
 XX  
 PR 19-MAY-2003; 2003CN-00123596.  
 XX  
 PA (TIAN/) TIAN J.  
 XX  
 PI Tian J, Gong Q;  
 XX  
 DR WPI; 2004-181274/18.  
 XX  
 PT Method for nucleic acid amplification detection, comprises using a line  
 PT probe and a ring probe and a one-step constant temperature reaction.  
 XX  
 PS Example 1; SEQ ID NO 3; 31pp; Chinese.  
 XX  
 CC This invention relates to a novel nucleic acid amplification detection  
 CC method. The invention can implement several operations of nucleic acid  
 CC hybridization, amplification and detection in the same reaction tube, by  
 CC only using one kind of DNA polymerase and by means of a one-step constant  
 CC temperature reaction. The invention is applicable to detection of RNA and  
 CC DNA. The present sequence is that of an oligonucleotide which was used in  
 CC the exemplification of the method of the invention.  
 XX  
 SQ Sequence 79 BP; 26 A; 18 C; 18 G; 17 T; 0 U; 0 Other;  
 Query Match 98.1%; Score 20.6; DB 13; Length 79;  
 Best Local Similarity 95.2%; Pred. No. 3.8;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CCCTGTGAGGAAGTCTGTCT 21  
 DB 41 CCCTGTGAGGAAGTCTGTCT 21  
 RESULT 34  
 ADP20411  
 ID ADP20411 standard; DNA; 80 BP.  
 XX  
 AC ADP20411;  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX  
 DE Hepatitis C virus IRES, region II sequence, SEQ ID 2.  
 XX  
 KW Virucide; Cytostatic; p110 subunit;  
 KW eukaryotic translation initiation factor eIF3; region II;  
 KW internal ribosome entry site; IRES; aminoglycoside;  
 KW hepatitis C infection; swine fever; bovine diarrhoea; viral infection;  
 KW cancer; ds.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN FR2848572-A1.  
 XX  
 PD 18-JUN-2004.  
 XX  
 PF 12-DEC-2002; 2002FR-00015718.  
 XX  
 PR 12-DEC-2002; 2002FR-00015718.  
 XX  
 PA (UYFO-) UNIV FOURIER JOSEPH.  
 XX  
 PI Balakireva L;  
 XX  
 DR WPI; 2004-452919/43.  
 XX  
 PT In vitro screening for antiviral agents, from ability to inhibit complex  
 PT formation between the p110 subunit of translation initiation factor eIF3  
 PT and region II of the viral internal ribosome binding site.



XX PS Claim 1; SEQ ID NO 2; 45pp; French.  
XX CC The present invention relates to an in vitro method of screening for  
CC compounds (A) that inhibit the formation of a complex between the p110  
CC subunit (ADP20413) of the eukaryotic translation initiation factor eIF3  
CC and region II of the internal ribosome entry site (IRES; ADP20411) of  
CC hepatitis C virus (HCV). Preferably the p110 recognition motif (ADP20414)  
CC and the region II consensus sequence (ADP20412), or fragment of it  
CC containing at least 8 consecutive nucleotides, are used. (A) is  
CC especially an aminoglycoside, specifically tobramycin or an  
CC oligonucleotide antisense to consensus sequence ADP20412, or parts of it.  
CC (A) are used for treating infection by hepatitis C, swine fever and  
CC bovine diarrhoea viruses, also for treating viral or non-viral diseases  
CC which involve proteins synthesis of which is initiated from an IRES, e.g.  
CC cancer.  
XX SQ Sequence 80 BP; 17 A; 21 C; 22 G; 20 T; 0 U; 0 Other;  
Query Match 98.1%; Score 20.6; DB 12; Length 80;  
Best Local Similarity 95.2%; Pred. No. 3.8;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CCCTGTGAGGAACCTWCTGTCT 21  
Db 4 CCCTGTGAGGAACCTWCTGTCT 24  
RESULT 35  
AAD33033  
ID AAD33033 standard; DNA; 85 BP.  
XX AC AAD33033;  
XX DT 01-JUL-2002 (first entry)  
XX DE HCV-S1 overlapping cDNA region amplifying sense PCR primer, H28.  
XX KW Nucleic acid construct; expression cassette; non-coding region; NCR;  
XX KW untranslated region; UTR; anti-viral drug; drug resistance; primer; PCR;  
XX KW HCV-S1; Hepatitis C virus; 88.  
XX OS Hepatitis C virus.  
XX PN WO200208447-A2.  
XX PD 31-JAN-2002.  
XX PF 20-JUL-2001; 2001WO-IL000669.  
XX PR 24-JUL-2000; 2000US-0220248P.  
XX PA (MOLE-) INST MOLECULAR & CELL BIOLOGY.  
XX PA (EHR/L) EHR/LICH G.  
XX PI Tan YH, Lim SP, Lim SG, Hong WJ;  
XX DR WPI; 2002-280605/32.  
XX PT Novel nucleic acid construct useful for detecting the presence of RNA  
XX virus, comprises an expression cassette and a promoter operably linked to  
XX expression cassette for minus strand RNA transcription of the cassette.  
XX PS Example 1; Page 24; 81pp; English.  
XX CC The invention relates to nucleic acid construct which comprises an  
XX expression cassette including a first polynucleotide region including a  
XX 5' non-coding region (NCR) sequence of an RNA virus and at least an N-  
XX terminal portion of a coding sequence of RNA virus, a second  
XX polynucleotide region including a 3' untranslated region (UTR) sequence  
XX of the RNA virus and at least a C-terminal portion of a coding sequence  
XX of the virus and a third polynucleotide region encoding a reporter  
XX molecule, flanked by first and second polynucleotide regions; and a

CC promoter sequence being operatively linked to expression cassette in a  
CC manner so as to enable a transcription of a minus strand RNA molecule  
CC from the expression cassette. Nucleic acid construct of the invention is  
CC useful for detecting the presence of an RNA virus in a cell. It is also  
CC useful for screening anti-viral drugs and determining drug resistance of  
CC an RNA virus. The present sequence is a PCR primer used to amplify the  
CC overlapping cDNA regions of the genome of Hepatitis C virus (HCV) isolate  
CC HCV-S1. Note: This sequence is stated to be same as that shown as SEQ ID  
CC NO:26 in the sequence listing of the specification, however this sequence  
XX has 2 additional bases at its 3' end  
XX SQ Sequence 85 BP; 20 A; 30 C; 20 G; 15 T; 0 U; 0 Other;  
Query Match 98.1%; Score 20.6; DB 6; Length 85;  
Best Local Similarity 95.2%; Pred. No. 3.8;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CCCTGTGAGGAACCTWCTGTCT 21  
Db 43 CCCTGTGAGGAACCTWCTGTCT 63  
RESULT 36  
ADW39165  
ID ADW39165 standard; DNA; 95 BP.  
XX AC ADW39165;  
XX DT 24-MAR-2005 (first entry)  
XX DE Novel nucleic acid amplification method-related oligonucleotide SeqID2.  
XX KW DNA detection; RNA detection; ss.  
XX OS Unidentified.  
XX PN CN1460722-A.  
XX PD 10-DEC-2003.  
XX PF 19-MAY-2003; 2003CN-00123596.  
XX PR 19-MAY-2003; 2003CN-00123596.  
XX PA (TIAN/) TIAN J.  
XX PI Tian J, Gong Q;  
XX DR WPI; 2004-181274/18.  
XX PT Method for nucleic acid amplification detection, comprises using a line  
XX probe and a ring probe and a one-step constant temperature reaction.  
XX PS Example 1; SEQ ID NO 2; 31pp; Chinese.  
XX CC This invention relates to a novel nucleic acid amplification detection  
XX method. The invention can implement several operations of nucleic acid  
XX hybridization, amplification and detection in the same reaction tube, by  
XX only using one kind of DNA polymerase and by means of a one-step constant  
XX temperature reaction. The invention is applicable to detection of RNA and  
XX DNA. The present sequence is that of an oligonucleotide which was used in  
XX the exemplification of the method of the invention.  
XX SQ Sequence 95 BP; 27 A; 26 C; 20 G; 22 T; 0 U; 0 Other;  
Query Match 98.1%; Score 20.6; DB 13; Length 95;  
Best Local Similarity 95.2%; Pred. No. 3.9;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CCCTGTGAGGAACCTWCTGTCT 21  
Db 43 CCCTGTGAGGAACCTWCTGTCT 63



Best Local Similarity 95.2%; Pred. No. 3.9; Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21  
|||||  
Db 11 CCCTGTGAGGAAGTCTGTCT 31

RESULT 39  
ABX03545  
ID ABX03545 standard; RNA; 127 BP.  
XX  
AC ABX03545;  
XX  
DT 07-JAN-2003 (first entry)  
XX  
DE Hepatitis C virus 1969 RNA UTR sequence.  
XX  
KW HCV; hepatitis C virus; NS3 protease; virucide; ss; helicase-inhibitor;  
KW infection.  
XX  
OS Hepatitis C virus.  
XX  
FH Key Location/Qualifiers  
FT stem\_loop 5..20  
FT /tag= a  
FT misc\_binding 44..52  
FT /tag= b  
FT /bound\_moiety= "Binds to nucleotides 118..111"  
FT misc\_binding 56..60  
FT /tag= c  
FT /bound\_moiety= "Binds to nucleotides 107..104"  
FT misc\_binding 65..70  
FT /tag= d  
FT /bound\_moiety= "Binds to nucleotides 102..97"  
FT stem\_loop 74..92  
FT /tag= e  
FT misc\_binding 97..102  
FT /tag= f  
FT /bound\_moiety= "Binds to nucleotides 70..65"  
FT misc\_binding 104..107  
FT /tag= g  
FT /bound\_moiety= "Binds to nucleotides 60..56"  
FT misc\_binding 111..118  
FT /tag= h  
FT /bound\_moiety= "Binds to nucleotides 52..44"  
XX  
PN WO200270752-A1.  
XX  
PD 12-SEP-2002.  
XX  
PF 14-FEB-2002; 2002WO-US004916.  
XX  
PR 14-FEB-2001; 2001US-0269776P.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Dasgupta A, Banerjee R;  
XX  
DR WPI; 2002-707103/76.  
XX  
PT Assaying a sample containing or suspected of containing hepatitis C virus (HCV) RNA for treating HCV infection comprises measuring the presence of the HCV RNA in the sample that binds to NS3.  
XX  
PS Example 2; Fig 3; 66pp; English.  
XX  
CC This invention relates to a novel method for assaying a sample containing or suspected of containing hepatitis C virus (HCV) RNA. The method comprises contacting the sample with an NS3 protease protein or its fragment or mutant to form a nucleoprotein complex, and measuring the amount or presence of the HCV RNA in the sample that binds to NS3. The method of the invention may have virucide activity and it may act as a

CC helicase-inhibitor-NS3. The method of the invention is useful for treating HCV infection. The present sequence represents an RNA sequence representing a mutant form of the HCV 1969 DNA 3' UTR used in the method of the invention  
XX  
SQ Sequence 127 BP; 26 A; 44 C; 32 G; 0 T; 25 U; 0 Other;  
Query Match 98.1%; Score 20.6; DB 6; Length 127;  
Best Local Similarity 66.7%; Pred. No. 4;  
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CCCTGTGAGGAAGTCTGTCT 21  
|||||  
Db 43 CCCTGTGAGGAAGTCTGTCT 63

RESULT 40  
ADM15169  
ID ADM15169 standard; DNA; 131 BP.  
XX  
AC ADM15169;  
XX  
DT 07-APR-2005 (first entry)  
XX  
DE HCV H77C RT-PCR product #3.  
XX  
KW Cell culture; Hepatitis C virus infection; gastrointestinal disease; infection; drug screening; ss; virucide; gene therapy;  
KW reverse transcriptase PCR.  
XX  
OS Hepatitis C virus; strain H77C.  
XX  
PN WO2005005625-A2.  
XX  
PD 20-JAN-2005.  
XX  
PF 14-JUL-2004; 2004WO-CA001009.  
XX  
PR 14-JUL-2003; 2003CA-02436104.  
XX  
PR 06-FEB-2004; 2004CA-02454540.  
XX  
PA (UYMC-) UNIV MCGILL.  
XX  
PI Sonnenberg N, Lopez Lastra M;  
XX  
DR WPI; 2005-122423/13.  
XX  
PT Generating an established cell line that produces hepatitis C virus (HCV) for identifying a compound with anti-HCV activity, comprises transforming peripheral blood mononuclear cells that produce HCV with Epstein Barr virus.  
XX  
PS Disclosure; Fig 57; 161pp; English.  
XX  
CC The invention relates to generating an established cell line that produces hepatitis C virus (HCV) comprising transforming peripheral blood mononuclear cells (PBMCs) that produce HCV with Epstein Barr virus (EBV). Also included are a method for producing HCV in vitro, an EBV-established B-cell line capable of replicating complete and infectious HCV, a cell-based in vitro replication system for HCV (comprising an EBV-transformed B-cell capable of replicating complete and infectious HCV and a second population having HCV tropism and in which robust HCV replication occurs, so that under appropriate culture conditions the second population can become infected by the infectious HCV produced by the EBV-transformed B-cell), an assay for screening a test agent and selecting an agent that possesses anti-HCV activity and a method for identifying a compound with anti-HCV activity from a library of compounds. The method is useful in generating an established cell line that produces hepatitis C virus (HCV) for identifying a compound with anti-HCV activity. HCV sequence was amplified by reverse transcription from EBV-immortalized cells (derived from patient PBMC samples) and compared to sequence amplified from the infectious strain H77C. The present sequence is a PCR amplicon from the control H77C virus.

```
XX SQ Sequence 131 BP; 27 A; 41 C; 37 G; 26 T; 0 U; 0 Other;
Query Match 98.1%; Score 20.6; DB 14; Length 131;
Best Local Similarity 95.2%; Pred. No. 4;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGAACTWCTGTCT 21
    |||||
DB 6 CCCTGTGAGGAAGAACTACTGTCT 26

RESULT 41
ADW15171
ID ADW15171 standard; DNA; 131 BP.
XX
AC ADW15171;
XX
DT 07-APR-2005 (first entry)
XX
DE HCV from immortalized cell line 9.a RT-PCR product #1.
XX
DE Cell culture; Hepatitis C virus infection; gastrointestinal disease;
KW infection; drug screening; ss; virucide; gene therapy;
KW reverse transcriptase PCR.
XX
OS Hepatitis C virus.
XX
PN WO2005005625-A2.
XX
PD 20-JAN-2005.
XX
PF 14-JUL-2004; 2004WO-CA001009.
XX
PR 14-JUL-2003; 2003CA-02436104.
PR 06-FEB-2004; 2004CA-02454540.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Sonenberg N, Lopez Lastra M;
XX
WPI; 2005-122423/13.
XX
PT Generating an established cell line that produces hepatitis C virus (HCV)
PT for identifying a compound with anti-HCV activity, comprises transforming
PT peripheral blood mononuclear cells that produce HCV with Epstein Barr
PT virus.
XX
PS Disclosure; Fig 57; 161pp; English.
XX
CC The invention relates to generating an established cell line that
CC produces hepatitis C virus (HCV) comprising transforming peripheral blood
CC mononuclear cells (PBMCs) that produce HCV with Epstein Barr virus (EBV).
CC Also included are a method for producing HCV in vitro, an EBV-established
CC B-cell line capable of replicating complete and infectious HCV, a cell-
CC based in vitro replication system for HCV (comprising an EBV-transformed
CC B-cell capable of replicating complete and infectious HCV and a second
CC population having HCV tropism and in which robust HCV replication occurs,
CC so that under appropriate culture conditions the second population can
CC become infected by the infectious HCV produced by the EBV-transformed B-
CC cell), an assay for screening a test agent and selecting an agent that
CC possesses anti-HCV activity and a method for identifying a compound with
CC anti-HCV activity from a library of compounds. The method is useful in
CC generating an established cell line that produces hepatitis C virus (HCV)
CC for identifying a compound with anti-HCV activity. HCV sequence was
CC amplified by reverse transcription from EBV-immortalized cell line 9.2
CC (derived from patient PBMC samples), passaged through several changes in
CC culture medium (designated 9.2a-9.2d cells) and compared to sequence
CC amplified from the infectious strain H77C. The present sequence is a PCR
CC amplicon from the HCV sequence amplified from EBV cell line 9.2a.
XX
SQ Sequence 131 BP; 27 A; 41 C; 37 G; 26 T; 0 U; 0 Other;
```

```
Query Match 98.1%; Score 20.6; DB 14; Length 131;
Best Local Similarity 95.2%; Pred. No. 4;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGAACTWCTGTCT 21
    |||||
DB 6 CCCTGTGAGGAAGAACTACTGTCT 26

RESULT 42
ADW15170
ID ADW15170 standard; DNA; 131 BP.
XX
AC ADW15170;
XX
DT 07-APR-2005 (first entry)
XX
DE HCV from immortalized cell line 9.2 RT-PCR product #1.
XX
DE Cell culture; Hepatitis C virus infection; gastrointestinal disease;
KW infection; drug screening; ss; virucide; gene therapy;
KW reverse transcriptase PCR.
XX
OS Hepatitis C virus.
XX
PN WO2005005625-A2.
XX
PD 20-JAN-2005.
XX
PF 14-JUL-2004; 2004WO-CA001009.
XX
PR 14-JUL-2003; 2003CA-02436104.
PR 06-FEB-2004; 2004CA-02454540.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Sonenberg N, Lopez Lastra M;
XX
WPI; 2005-122423/13.
XX
PT Generating an established cell line that produces hepatitis C virus (HCV)
PT for identifying a compound with anti-HCV activity, comprises transforming
PT peripheral blood mononuclear cells that produce HCV with Epstein Barr
PT virus.
XX
PS Disclosure; Fig 57; 161pp; English.
XX
CC The invention relates to generating an established cell line that
CC produces hepatitis C virus (HCV) comprising transforming peripheral blood
CC mononuclear cells (PBMCs) that produce HCV with Epstein Barr virus (EBV).
CC Also included are a method for producing HCV in vitro, an EBV-established
CC B-cell line capable of replicating complete and infectious HCV, a cell-
CC based in vitro replication system for HCV (comprising an EBV-transformed
CC B-cell capable of replicating complete and infectious HCV and a second
CC population having HCV tropism and in which robust HCV replication occurs,
CC so that under appropriate culture conditions the second population can
CC become infected by the infectious HCV produced by the EBV-transformed B-
CC cell), an assay for screening a test agent and selecting an agent that
CC possesses anti-HCV activity and a method for identifying a compound with
CC anti-HCV activity from a library of compounds. The method is useful in
CC generating an established cell line that produces hepatitis C virus (HCV)
CC for identifying a compound with anti-HCV activity. HCV sequence was
CC amplified by reverse transcription from EBV-immortalized cell line 9.2
CC (derived from patient PBMC samples), passaged through several changes in
CC culture medium (designated 9.2a-9.2d cells) and compared to sequence
CC amplified from the infectious strain H77C. The present sequence is a PCR
CC amplicon from the HCV sequence amplified from EBV cell line 9.2.
XX
SQ Sequence 131 BP; 27 A; 41 C; 37 G; 26 T; 0 U; 0 Other;
```

```
Query Match 98.1%; Score 20.6; DB 14; Length 131;
Best Local Similarity 95.2%; Pred. No. 4;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 CCTGTGAGGAAGTCTGTCT 21  
|||||  
Db 6 CCTGTGAGGAAGTCTGTCT 26

## RESULT 43

ADW15174  
ID ADW15174 standard; DNA; 131 BP.

XX AC ADW15174;

XX DT 07-APR-2005 (first entry)

XX DE HCV from immortalized cell line 9.2d RT-PCR product #1.

XX KW Cell culture; Hepatitis C virus infection; gastrointestinal disease;  
XX KW infection; drug screening; ss; virucide; gene therapy;  
XX KW reverse transcriptase PCR.

XX OS Hepatitis C virus.

XX PN WO2005005625-A2.

XX PD 20-JAN-2005.

XX PF 14-JUL-2004; 2004WO-CA001009.

XX PR 14-JUL-2003; 2003CA-02436104.

XX PR 06-FEB-2004; 2004CA-02454540.

XX PA (UYMC-) UNIV MCGILL.

XX PI Sonenberg N, Lopez Lastra M;

XX DR WPI; 2005-122423/13.

XX PT Generating an established cell line that produces hepatitis C virus (HCV)  
XX PT for identifying a compound with anti-HCV activity, comprises transforming  
XX PT peripheral blood mononuclear cells that produce HCV with Epstein Barr  
XX PT virus.

XX PS Disclosure; Fig 57; 161pp; English.

XX CC The invention relates to generating an established cell line that  
XX CC produces hepatitis C virus (HCV) comprising transforming peripheral blood  
XX CC mononuclear cells (PBMCs) that produce HCV with Epstein Barr virus (EBV).  
XX CC Also included are a method for producing HCV in vitro, an EBV-established  
XX CC B-cell line capable of replicating complete and infectious HCV, a cell-  
XX CC based in vitro replication system for HCV (comprising an EBV-transformed  
XX CC B-cell capable of replicating complete and infectious HCV and a second  
XX CC population having HCV tropism and in which robust HCV replication occurs,  
XX CC so that under appropriate culture conditions the second population can  
XX CC become infected by the infectious HCV produced by the EBV-transformed B-  
XX CC cell), an assay for screening a test agent and selecting an agent that  
XX CC possesses anti-HCV activity and a method for identifying a compound with  
XX CC anti-HCV activity from a library of compounds. The method is useful in  
XX CC generating an established cell line that produces hepatitis C virus (HCV)  
XX CC for identifying a compound with anti-HCV activity. HCV sequence was  
XX CC amplified by reverse transcription from EBV-immortalized cell line 9.2  
XX CC (derived from patient PBMC samples), passaged through several changes in  
XX CC culture medium (designated 9.2a-9.2d cells) and compared to sequence  
XX CC amplified from the infectious strain H77C. The present sequence is a PCR  
XX CC amplicon from the HCV sequence amplified from EBV cell line 9.2d.

XX SQ Sequence 131 BP; 27 A; 41 C; 37 G; 26 T; 0 U; 0 Other;

Query Match 98.1%; Score 20.6; DB 14; Length 131;  
Best Local Similarity 95.2%; Pred. No. 4;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21  
|||||

Db 6 CCTGTGAGGAAGTCTGTCT 26

## RESULT 44

ADW15172  
ID ADW15172 standard; DNA; 131 BP.

XX AC ADW15172;

XX DT 07-APR-2005 (first entry)

XX DE HCV from immortalized cell line 9.2b RT-PCR product #1.

XX KW Cell culture; Hepatitis C virus infection; gastrointestinal disease;  
XX KW infection; drug screening; ss; virucide; gene therapy;  
XX KW reverse transcriptase PCR.

XX OS Hepatitis C virus.

XX FH Key Location/Qualifiers  
XX FT mutation replace(70,G)  
XX FT mutation /\*tag= a

XX FT mutation replace(82,A)  
XX FT mutation /\*tag= b

XX PN WO2005005625-A2.

XX PD 20-JAN-2005.

XX PF 14-JUL-2004; 2004WO-CA001009.

XX PR 14-JUL-2003; 2003CA-02436104.

XX PR 06-FEB-2004; 2004CA-02454540.

XX PA (UYMC-) UNIV MCGILL.

XX PI Sonenberg N, Lopez Lastra M;

XX DR WPI; 2005-122423/13.

XX PT Generating an established cell line that produces hepatitis C virus (HCV)  
XX PT for identifying a compound with anti-HCV activity, comprises transforming  
XX PT peripheral blood mononuclear cells that produce HCV with Epstein Barr  
XX PT virus.

XX PS Disclosure; Fig 57; 161pp; English.

XX CC The invention relates to generating an established cell line that  
XX CC produces hepatitis C virus (HCV) comprising transforming peripheral blood  
XX CC mononuclear cells (PBMCs) that produce HCV with Epstein Barr virus (EBV).  
XX CC Also included are a method for producing HCV in vitro, an EBV-established  
XX CC B-cell line capable of replicating complete and infectious HCV, a cell-  
XX CC based in vitro replication system for HCV (comprising an EBV-transformed  
XX CC B-cell capable of replicating complete and infectious HCV and a second  
XX CC population having HCV tropism and in which robust HCV replication occurs,  
XX CC so that under appropriate culture conditions the second population can  
XX CC become infected by the infectious HCV produced by the EBV-transformed B-  
XX CC cell), an assay for screening a test agent and selecting an agent that  
XX CC possesses anti-HCV activity and a method for identifying a compound with  
XX CC anti-HCV activity from a library of compounds. The method is useful in  
XX CC generating an established cell line that produces hepatitis C virus (HCV)  
XX CC for identifying a compound with anti-HCV activity. HCV sequence was  
XX CC amplified by reverse transcription from EBV-immortalized cell line 9.2  
XX CC (derived from patient PBMC samples), passaged through several changes in  
XX CC culture medium (designated 9.2a-9.2d cells) and compared to sequence  
XX CC amplified from the infectious strain H77C. The present sequence is a PCR  
XX CC amplicon from the HCV sequence amplified from EBV cell line 9.2b.

XX SQ Sequence 131 BP; 27 A; 42 C; 36 G; 26 T; 0 U; 0 Other;

Query Match 98.1%; Score 20.6; DB 14; Length 131;  
Best Local Similarity 95.2%; Pred. No. 4;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGCT 21  
 DB 6 CCTGTGAGGAAGTCTGCT 26

RESULT 45  
 ADM15173  
 ID ADM15173 standard; DNA; 131 BP.

AC ADW15173;  
 XX 07-APR-2005 (first entry)  
 DT HCV from immortalized cell line 9.2c RT-PCR product #1.  
 DE Cell culture; Hepatitis C virus infection; gastrointestinal disease;  
 KW infection; drug screening; ss; virucide; gene therapy;  
 KW reverse transcriptase PCR.  
 XX Hepatitis C virus.  
 OS  
 PN WO2005005625-A2.  
 XX  
 XX 20-JAN-2005.  
 XX 14-JUL-2004; 2004WO-CA001009.  
 XX 14-JUL-2003; 2003CA-02436104.  
 PR 06-FEB-2004; 2004CA-02454540.  
 XX (UYMC-) UNIV MCGILL.  
 XX Sonenberg N, Lopez Lastra M;  
 PI WPI; 2005-122423/13.  
 XX  
 XX Generating an established cell line that produces hepatitis C virus (HCV)  
 PT for identifying a compound with anti-HCV activity, comprises transforming  
 PT peripheral blood mononuclear cells that produce HCV with Epstein Barr  
 PT virus.  
 XX  
 XX Disclosure; Fig 57; 161pp; English.

XX The invention relates to generating an established cell line that  
 CC produces hepatitis C virus (HCV) comprising transforming peripheral blood  
 CC mononuclear cells (PBMCs) that produce HCV with Epstein Barr virus (EBV).  
 CC Also included are a method for producing HCV in vitro, an EBV-established  
 CC B-cell line capable of replicating complete and infectious HCV, a cell-  
 CC based in vitro replication system for HCV (comprising an EBV-transformed  
 CC B-cell capable of replicating complete and infectious HCV and a second  
 CC population having HCV tropism and in which robust HCV replication occurs,  
 CC so that under appropriate culture conditions the second population can  
 CC become infected by the infectious HCV produced by the EBV-transformed B-  
 CC cell), an assay for screening a test agent and selecting an agent that  
 CC possesses anti-HCV activity and a method for identifying a compound with  
 CC anti-HCV activity from a library of compounds. The method is useful in  
 CC generating an established cell line that produces hepatitis C virus (HCV)  
 CC for identifying a compound with anti-HCV activity. HCV sequence was  
 CC amplified by reverse transcription from EBV-immortalized cell line 9.2  
 CC (derived from patient PBMC samples), passaged through several changes in  
 CC culture medium (designated 9.2a-9.2d cells) and compared to sequence  
 CC amplified from the infectious strain H77C. The present sequence is a PCR  
 CC amplicon from the HCV sequence amplified from EBV cell line 9.2c.

XX Sequence 131 BP; 27 A; 41 C; 37 G; 26 T; 0 U; 0 Other;  
 SQ Query Match 98.1%; Score 20.6; DB 14; Length 131;  
 Best Local Similarity 95.2%; Pred. No. 4;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGCT 21  
 DB 6 CCTGTGAGGAAGTCTGCT 26

RESULT 45  
 ADM15173  
 ID ADM15173 standard; DNA; 131 BP.

AC ADW15173;  
 XX 07-APR-2005 (first entry)  
 DT HCV from immortalized cell line 9.2c RT-PCR product #1.  
 DE Cell culture; Hepatitis C virus infection; gastrointestinal disease;  
 KW infection; drug screening; ss; virucide; gene therapy;  
 KW reverse transcriptase PCR.  
 XX Hepatitis C virus.  
 OS  
 PN WO2005005625-A2.  
 XX  
 XX 20-JAN-2005.  
 XX 14-JUL-2004; 2004WO-CA001009.  
 XX 14-JUL-2003; 2003CA-02436104.  
 PR 06-FEB-2004; 2004CA-02454540.  
 XX (UYMC-) UNIV MCGILL.  
 XX Sonenberg N, Lopez Lastra M;  
 PI WPI; 2005-122423/13.  
 XX  
 XX Generating an established cell line that produces hepatitis C virus (HCV)  
 PT for identifying a compound with anti-HCV activity, comprises transforming  
 PT peripheral blood mononuclear cells that produce HCV with Epstein Barr  
 PT virus.  
 XX  
 XX Disclosure; Fig 57; 161pp; English.

XX The invention relates to generating an established cell line that  
 CC produces hepatitis C virus (HCV) comprising transforming peripheral blood  
 CC mononuclear cells (PBMCs) that produce HCV with Epstein Barr virus (EBV).  
 CC Also included are a method for producing HCV in vitro, an EBV-established  
 CC B-cell line capable of replicating complete and infectious HCV, a cell-  
 CC based in vitro replication system for HCV (comprising an EBV-transformed  
 CC B-cell capable of replicating complete and infectious HCV and a second  
 CC population having HCV tropism and in which robust HCV replication occurs,  
 CC so that under appropriate culture conditions the second population can  
 CC become infected by the infectious HCV produced by the EBV-transformed B-  
 CC cell), an assay for screening a test agent and selecting an agent that  
 CC possesses anti-HCV activity and a method for identifying a compound with  
 CC anti-HCV activity from a library of compounds. The method is useful in  
 CC generating an established cell line that produces hepatitis C virus (HCV)  
 CC for identifying a compound with anti-HCV activity. HCV sequence was  
 CC amplified by reverse transcription from EBV-immortalized cell line 9.2  
 CC (derived from patient PBMC samples), passaged through several changes in  
 CC culture medium (designated 9.2a-9.2d cells) and compared to sequence  
 CC amplified from the infectious strain H77C. The present sequence is a PCR  
 CC amplicon from the HCV sequence amplified from EBV cell line 9.2c.

XX Sequence 131 BP; 27 A; 41 C; 37 G; 26 T; 0 U; 0 Other;  
 SQ Query Match 98.1%; Score 20.6; DB 14; Length 131;  
 Best Local Similarity 95.2%; Pred. No. 4;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 6 CCTGTGAGGAAGTCTGCT 26

RESULT 46  
 AAZ57175  
 ID AAZ57175 standard; RNA; 133 BP.

XX AAZ57175;  
 AC AAZ57175;  
 XX 27-MAR-2000 (first entry)  
 DT Human hepatitis C virus containing 133 mer RNA sequence.

DE Bacteriophage SP6 promoter; single stranded RNA assay; diagnosis;  
 XX infectious disease; gene cloning; viral RNA; bacterial mRNA; ss.  
 KW Hepatitis C virus.  
 OS Synthetic.  
 XX EP969101-A1.  
 PN 05-JAN-2000.  
 XX 01-JUL-1999; 99EP-00112731.  
 XX 01-JUL-1998; 98JP-00186434.  
 PR (TOYJ) TOSOH CORP.  
 XX Ishiguro T, Saitoh J, Ishizuka T;  
 PI WPI; 2000-089306/08.  
 XX  
 XX Assaying single stranded RNA, to diagnose infectious diseases and to  
 PT determine the effects of therapeutic agents on the infectious diseases.  
 PT Example 6; Page 13; 39pp; English.

XX A method has been developed for the assay of a single stranded RNA  
 CC containing a specific nucleic acid sequence in a sample at almost  
 CC constant temperature. The method is used to detect and quantify viral RNA  
 CC and bacterial mRNA and is used for diagnosis of infectious diseases and  
 CC in judging the effects of therapeutic agents for the infectious diseases.  
 CC Large amounts of DNA and RNA can be produced containing a specific  
 CC nucleic acid sequence which is useful for cloning genes and exploring the  
 CC unknown genes. The present sequence is used in the exemplification of the  
 CC present invention  
 XX Sequence 133 BP; 30 A; 40 C; 36 G; 0 T; 27 U; 0 Other;  
 SQ Query Match 98.1%; Score 20.6; DB 3; Length 133;  
 Best Local Similarity 66.7%; Pred. No. 4;  
 Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGCT 21  
 DB 93 CCUGUGAGGAACUACUGUCU 113

RESULT 47  
 AAZ57775/C  
 ID AAZ57775 standard; DNA; 155 BP.

XX AAZ57775;  
 AC AAZ57775;  
 XX 05-APR-2000 (first entry)  
 DT Hepatitis C virus antisense inhibitor oligonucleotide #41.

DE Hepatitis C virus; HCV; antisense oligonucleotide; hepatotropic; ss;  
 KW anti-inflammatory; translation inhibition; HCV infection; virucide.  
 XX Hepatitis C virus.  
 OS

XX US6001990-A.  
XX 14-DEC-1999.  
XX 07-JUN-1995; 95US-00474700.  
XX 10-MAY-1994; 94US-00240382.  
XX (GEO) GEN HOSPITAL CORP.  
XX Moradpour D, Wands JR, Wakita T;  
XX WPI; 2000-104900/09.  
XX Antisense oligonucleotide to Hepatitis C virus RNA, useful for treating  
PT Hepatitis C virus infections.  
XX Claim 30; Col 33; 31pp; English.  
XX This sequence is an antisense oligonucleotide that hybridizes to  
CC Hepatitis C virus (HCV) RNA, under physiological conditions. The  
CC invention relates to HCV antisense oligonucleotides, and also for a  
CC vector comprising a nucleotide sequence which is transcribed in an animal  
CC cell to generate an antisense oligonucleotide. The oligonucleotides have  
CC virucide, hepatotropic and anti-inflammatory activity, and are useful for  
CC treating HCV infection by inhibiting translation of type I-V HCV RNA.  
CC Hepatitis C virus is a positive strand RNA virus, and is the major  
CC causative agent of post-transfusion hepatitis. Persistent HCV infection  
CC can lead to chronic hepatitis, cirrhosis, and hepatocellular carcinoma  
XX Sequence 155 BP; 29 A; 43 C; 51 G; 32 T; 0 U; 0 Other;  
SQ Query Match 98.1%; Score 20.6; DB 3; Length 155;  
Best Local Similarity 95.2%; Pred. No. 4.1;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CCTGTGAGGAAGTCTGTCT 21  
DB 113 CCTGTGAGGAAGTCTGTCT 93  
RESULT 48  
AD05716  
ID ADR05716 standard; RNA; 210 BP.  
XX ADR05716;  
XX 04-NOV-2004 (first entry)  
XX Hepatitis C virus UTR domain II-IIIb RNA fragment SEQ ID NO:29.  
DE screening; identification; RNA regulatory element; reporter mRNA;  
KW medicine; gene expression modulation; Hepatitis C virus; HCV;  
KW untranslated region; UTR; gene; ss.  
OS Hepatitis C virus.  
XX WO2004067728-A2.  
XX 12-AUG-2004.  
XX 09-JAN-2004; 2004WO-US000423.  
XX 17-JAN-2003; 2003US-0441028P.  
XX (PTCT-) PTC THERAPEUTICS.  
XX Pellegrini MC, Trotta CR, Huq SI;  
PI WPI; 2004-581000/56.  
DR Screening for and/or identifying (non-cell based) an RNA regulatory  
PT

PT element comprises combining a translation extract, an RNA test sequence,  
PT and a reporter mRNA under conditions suitable for translation of the  
PT reporter mRNA.  
XX Example 2; SEQ ID NO 29; 87pp; English.  
XX The present invention describes a non-cell based method of screening for  
CC and/or identifying an RNA regulatory element. The method comprises  
CC combining a translation extract, an RNA test sequence, and a reporter  
CC mRNA under conditions suitable for translation of the reporter mRNA, and  
CC measuring the effect of the test sequence on the translation of the  
CC reporter mRNA, where a test sequence that modifies the translation of the  
CC reporter mRNA includes an RNA regulatory element. Also described: (1) a  
CC non-cell based method of screening for and/or identifying at least one  
CC test compound which modulates the ability of an RJSTa sequence to  
CC regulate translation of a reporter mRNA; (2) an in vitro translation  
CC system for screening for and/or identifying a test compound, which  
CC modulates the ability of an RNA regulatory sequence to regulate  
CC translation of a reporter mRNA; (3) screening for and/or identifying a  
CC test compound, which modulates the ability of an RNA regulatory sequence  
CC to regulate translation of a reporter mRNA; (4) an in vitro translation  
CC system for screening for and/or identifying a test compound capable of  
CC reversing the inhibition of translation mediated by an RNA regulatory  
CC sequence; (4) screening for and/or identifying a test compound, which  
CC reverses inhibition of translation; and (5) a test compound identified  
CC according to the method described above. The methods and systems are  
CC useful for screening for and/or identifying an RNA regulatory element.  
CC The test compound is useful for the manufacture of a medicine for  
CC modulating the expression of a gene comprising the RNA sequence or of the  
CC protein expressed from a construct engineered to include the RNA  
CC sequence. The expression of the gene is aberrant in a disease state that  
CC causes the survival and/or progression of a pathogenic organism. The  
CC present sequence represents a Hepatitis C virus untranslated region (UTR)  
CC RNA fragment, which is used in the exemplification of the present  
CC invention.  
XX Sequence 210 BP; 45 A; 64 C; 55 G; 0 T; 46 U; 0 Other;  
SQ Query Match 98.1%; Score 20.6; DB 13; Length 210;  
Best Local Similarity 66.7%; Pred. No. 4.2;  
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CCTGTGAGGAAGTCTGTCT 21  
DB 26 CCUGUGAGGAACUACUGUCU 46  
RESULT 49  
AD05719  
ID ADR05719 standard; RNA; 235 BP.  
XX ADR05719;  
XX 04-NOV-2004 (first entry)  
XX Hepatitis C virus UTR domain II-IIIabc RNA fragment SEQ ID NO:32.  
DE screening; identification; RNA regulatory element; reporter mRNA;  
KW medicine; gene expression modulation; Hepatitis C virus; HCV;  
KW untranslated region; UTR; gene; ss.  
OS Hepatitis C virus.  
XX WO2004067728-A2.  
XX 12-AUG-2004.  
XX 09-JAN-2004; 2004WO-US000423.  
XX 17-JAN-2003; 2003US-0441028P.  
XX (PTCT-) PTC THERAPEUTICS.  
XX





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OM nucleic - nucleic search, using sw model

Run on: January 27, 2006, 03:55:23 ; Search time 894 Seconds  
(without alignments)  
1335.249 Million cell updates/sec

Title: US-10-070-415A-1

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Sequence: 1 ccctgtgaggaaactwtgtct 21

Scoring table: IDENTITY\_NUC  
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Searched: 5893141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

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1: gb\_ba.\*  
2: gb\_in.\*  
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5: gb\_ov.\*  
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7: gb\_ph.\*  
8: gb\_pr.\*  
9: gb\_ro.\*  
10: gb\_sts.\*  
11: gb\_sv.\*  
12: gb\_un.\*  
13: gb\_vl.\*  
14: gb\_htg.\*  
15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20.6	98.1	21	6	BD178495
2	20.6	98.1	21	6	BD182888
3	20.6	98.1	24	6	AX003352
4	20.6	98.1	24	6	AX470074
5	20.6	98.1	24	6	AX470078
6	20.6	98.1	24	6	AX470079
7	20.6	98.1	25	6	AR593796
8	20.6	98.1	27	6	A39029
9	20.6	98.1	27	6	AR063363
10	20.6	98.1	27	6	AR123554
11	20.6	98.1	27	6	AR267295
12	20.6	98.1	27	6	AR305705
13	20.6	98.1	27	6	AR654197
14	20.6	98.1	27	6	AR655174
15	20.6	98.1	27	6	AX023091
16	20.6	98.1	27	6	AX398128
17	20.6	98.1	27	6	AX417297
18	20.6	98.1	28	6	AR094964

19	20.6	98.1	28	6	AR094991
20	20.6	98.1	31	6	E11709
21	20.6	98.1	45	6	BD069486
22	20.6	98.1	45	6	BD083958
23	20.6	98.1	45	6	AR338407
24	20.6	98.1	45	6	AR353602
25	20.6	98.1	45	6	AR636812
26	20.6	98.1	51	6	I73300
27	20.6	98.1	67	6	AR095004
28	20.6	98.1	73	6	BD171247
29	20.6	98.1	80	6	CQ830528
30	20.6	98.1	131	13	CS001589
31	20.6	98.1	131	13	CS001590
32	20.6	98.1	131	13	CS001591
33	20.6	98.1	131	13	CS001592
34	20.6	98.1	131	13	CS001593
35	20.6	98.1	131	13	CS001594
36	20.6	98.1	155	6	AR095003
37	20.6	98.1	232	13	AF506627
38	20.6	98.1	232	13	AF506629
39	20.6	98.1	232	13	AF506666
40	20.6	98.1	232	13	AF506679
41	20.6	98.1	238	6	BD182732
42	20.6	98.1	238	6	BD182733
43	20.6	98.1	238	6	BD182735
44	20.6	98.1	238	13	AF506647
45	20.6	98.1	238	13	AF506655
46	20.6	98.1	239	6	BD182734
47	20.6	98.1	239	13	AF506683
48	20.6	98.1	242	13	AF506687
49	20.6	98.1	258	13	AY344040
50	20.6	98.1	260	6	AR095002
51	20.6	98.1	260	6	AR655260
52	20.6	98.1	260	6	AR655261
53	20.6	98.1	260	6	AR655262
54	20.6	98.1	260	6	AR655263
55	20.6	98.1	265	13	CS001586
56	20.6	98.1	266	13	CS001585
57	20.6	98.1	267	6	AX398192
58	20.6	98.1	278	6	AX398190
59	20.6	98.1	280	13	AY344026
60	20.6	98.1	291	13	HPCSNOCR
61	20.6	98.1	296	13	HPCBR56A
62	20.6	98.1	297	13	AY435124
63	20.6	98.1	299	6	AX171760
64	20.6	98.1	299	13	AY7344478S1
65	20.6	98.1	301	13	AY033769
66	20.6	98.1	304	13	HCUS9514
67	20.6	98.1	304	13	HPCHCNJ4
68	20.6	98.1	305	6	I40293
69	20.6	98.1	305	6	I59670
70	20.6	98.1	305	6	AX398186
71	20.6	98.1	305	6	AX398187
72	20.6	98.1	305	6	AX398188
73	20.6	98.1	305	6	AX398189
74	20.6	98.1	305	6	AX398191
75	20.6	98.1	306	6	E07741
76	20.6	98.1	308	6	AR118714
77	20.6	98.1	308	6	AR118715
78	20.6	98.1	308	6	AR118716
79	20.6	98.1	308	6	AR118717
80	20.6	98.1	308	6	AR118718
81	20.6	98.1	308	6	AR118719
82	20.6	98.1	308	6	AR118720
83	20.6	98.1	318	6	BD182731
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85	20.6	98.1	324	6	AR027770
86	20.6	98.1	324	6	AR027784
87	20.6	98.1	327	13	AY8344219
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90	20.6	98.1	328	6	AX419905
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92 20.6 98.1 328 6 AX419908 Sequence  
 93 20.6 98.1 332 6 E08277 cDNA encodi  
 94 20.6 98.1 340 13 HPC5NR4 D31604 Human hepat  
 95 20.6 98.1 340 13 HPC5NR5 D31605 Human hepat  
 96 20.6 98.1 340 13 HPC5NRE D29819 Hepatitis C  
 97 20.6 98.1 341 6 AR119855 Sequence  
 98 20.6 98.1 341 6 AR119856 Sequence  
 99 20.6 98.1 341 6 AR119857 Sequence  
 100 20.6 98.1 341 6 AR153763 Sequence

## ALIGNMENTS

RESULT 1  
 BD178495  
 LOCUS 21 bp DNA linear PAT 16-APR-2003  
 DEFINITION Method of detecting nucleic acid relating to disease.  
 ACCESSION BD178495  
 VERSION BD178495.1 GI:30015761  
 KEYWORDS WO 02077281-A/1.  
 SOURCE unidentified  
 ORGANISM unclassified.  
 1 (bases 1 to 21)  
 Hashimoto,K., Hashimoto,M., Mishiro,S. and Ota,Y.  
 Method of detecting nucleic acid relating to disease  
 Patent: WO 02077281-A 1 03-OCT-2002;  
 TOSHIBA CORP, KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO,  
 YASUHIKO OTA

COMMENT OS Hepatitis virus (hepatitis C virus)  
 PN WO 02077281-A/1  
 PD 03-OCT-2002  
 PF 05-MAR-2002 WO 2002JP002030  
 PR 27-MAR-2001 JP 01P 090053.18-SEP-2001 JP 01P 284112 PI  
 KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO, YASUHIKO OTA PC  
 C12Q1/68, C12N15/09, C12M1/00, G01N33/53, G01N33/543, G01N33/566, PC  
 G01N33/576,  
 PC G01N37/00  
 CC Method of detecting nucleic acid relating to disease FH Key  
 FT source Location/Qualifiers  
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 QY 1 CCCTGTGAGGAAGTCTGTCT 21  
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 Db 1 CCCTGTGAGGAAGTCTGTCT 21

RESULT 2  
 BD182888  
 LOCUS 21 bp DNA linear PAT 17-JUN-2003  
 DEFINITION Detection of nucleic acid associated with disease.  
 ACCESSION BD182888  
 VERSION BD182888.1 GI:31875088  
 KEYWORDS JP 2002355083-A/1.  
 SOURCE unidentified  
 ORGANISM unclassified.  
 1 (bases 1 to 21)  
 Hashimoto,K., Hashimoto,M., Mishiro,S. and Ota,Y.  
 Detection of nucleic acid associated with disease

REFERENCE  
 AUTHORS Hashimoto,K., Hashimoto,M., Mishiro,S. and Ota,Y.  
 TITLE Detection of nucleic acid associated with disease

JOURNAL  
COMMENT

Patent: JP 2002355083-A 1 10-DEC-2002;  
 TOSHIBA CORP  
 OS Hepatitis virus (hepatitis C virus)  
 PN JP 2002355083-A/1  
 PD 10-DEC-2002  
 PF 26-MAR-2002 JP 2002086681  
 PI KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO, YASUHIKO OTA PC  
 C12N15/09, C12N15/09, C12M1/00, C12Q1/68, G01N33/53, G01N33/566, PC  
 G01N33/569,  
 PC G01N33/576// (C12Q1/68, C12R1/93), C12N15/00, C12N15/00 CC  
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source

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## ORIGIN

Query Match 98.1%; Score 20.6; DB 6; Length 21;  
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 Db 1 CCCTGTGAGGAAGTCTGTCT 21

RESULT 3  
 AX003352  
 LOCUS 24 bp DNA linear PAT 24-AUG-2000  
 DEFINITION Sequence 3 from Patent WO9928503.  
 ACCESSION AX003352  
 VERSION AX003352.1 GI:9927157  
 KEYWORDS  
 SOURCE Hepatitis C virus  
 ORGANISM Hepatitis C virus  
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 Hepacivirus.

REFERENCE  
 AUTHORS Primi,D. and Mantero,G.  
 TITLE Methods of detecting polynucleotide analytes  
 JOURNAL Patent: WO 9928503-A 3 10-JUN-1999;  
 PRIMI DANIELE (IT); MANTERO GIOVANNI (IT)

FEATURES  
source

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 /organism="Hepatitis C virus"  
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## ORIGIN

Query Match 98.1%; Score 20.6; DB 6; Length 24;  
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 QY 1 CCCTGTGAGGAAGTCTGTCT 21  
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 Db 2 CCCTGTGAGGAAGTCTGTCT 22

## RESULT 4

AX470074  
 LOCUS 24 bp DNA linear PAT 09-AUG-2002  
 DEFINITION Sequence 1 from Patent WO02052041.  
 ACCESSION AX470074  
 VERSION AX470074.1 GI:22205310  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 other sequences, artificial sequences.

REFERENCE 1  
AUTHORS Gessner, M.  
TITLE 5' nuclease nucleic acid amplification assay having an improved internal control  
JOURNAL Patent: WO 02052041-A 1 04-JUL-2002;  
Baxter Aktiengesellschaft (AT)  
FEATURES Location/Qualifiers  
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Qy 1 CCCTGTGAGGAACCTGCTCT 21  
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Db 1 CCCTGTGAGGAACCTGCTCT 21

RESULT 5  
AX470078 24 bp DNA linear PAT 09-AUG-2002  
LOCUS  
DEFINITION Sequence 5 from Patent WO02052041.  
ACCESSION AX470078  
VERSION AX470078.1 GI:22205314  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Gessner, M.  
TITLE 5' nuclease nucleic acid amplification assay having an improved internal control  
JOURNAL Patent: WO 02052041-A 5 04-JUL-2002;  
Baxter Aktiengesellschaft (AT)  
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/db\_xref="taxon:32630"  
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ORIGIN

Query Match 98.1%; Score 20.6; DB 6; Length 24;  
Best Local Similarity 95.2%; Pred. No. 5;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAACCTGCTCT 21  
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Db 1 CCCTGTGAGGAACCTGCTCT 21

RESULT 6  
AX470079 24 bp DNA linear PAT 09-AUG-2002  
LOCUS  
DEFINITION Sequence 6 from Patent WO02052041.  
ACCESSION AX470079  
VERSION AX470079.1 GI:22205315  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Gessner, M.  
TITLE 5' nuclease nucleic acid amplification assay having an improved internal control  
JOURNAL Patent: WO 02052041-A 6 04-JUL-2002;  
Baxter Aktiengesellschaft (AT)  
FEATURES Location/Qualifiers

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Best Local Similarity 95.2%; Pred. No. 5;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAACCTGCTCT 21  
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Db 1 CCCTGTGAGGAACCTGCTCT 21

RESULT 7  
AR593796 25 bp DNA linear PAT 15-DEC-2004  
LOCUS  
DEFINITION Sequence 1 from patent US 6811974.  
ACCESSION AR593796  
VERSION AR593796.1 GI:56643301  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Hu, Y.-W.  
TITLE Primer-specific and mismatch extension assay for identifying gene variation  
JOURNAL Patent: US 6811974-A 1 02-NOV-2004;  
Canadian Blood Services; Ottawa; CAX;  
FEATURES Location/Qualifiers  
source 1..25  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 98.1%; Score 20.6; DB 6; Length 25;  
Best Local Similarity 95.2%; Pred. No. 5;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAACCTGCTCT 21  
|||||:|||||:|||||  
Db 4 CCCTGTGAGGAACCTGCTCT 24

RESULT 8  
A39029 27 bp DNA linear PAT 05-MAR-1997  
LOCUS  
DEFINITION Sequence 1 from Patent WO9412670.  
ACCESSION A39029  
VERSION A39029.1 GI:2295415  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
unclassified sequences.  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Maertens, G., Stuyver, L., Rossau, R. and Van, H.H.  
TITLE PROCESS FOR TYPING OF HCV ISOLATES  
JOURNAL Patent: WO 9412670-A 1 09-JUN-1994;  
INNOGENETICS NV (BE)  
COMMENT Other publication AU 5628294 940622  
Other publication CA 2128528 940609  
Other publication JP 7501437 950406.  
FEATURES Location/Qualifiers  
source 1..27  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

ORIGIN

Fri Jan 27 09:12:34 2006

Query Match	98.1%;	Score 20.6;	DB 6;	Length 27;		
Best Local Similarity	100.0%;	Pred. No. 4.9;				
Matches	21;	Conservative	0;	Mismatches	0;	
			Indels	0;	Gaps	0;
QY	1	CCCTGTGAGGAAGTCTGTCT 21				
Db	1	CCCTGTGAGGAAGTCTGTCT 21				
RESULT 9						
LOCUS	AR063363	27 bp	DNA	linear	PAT 29-SEP-1999	
DEFINITION	Sequence 1 from patent US 5846704.					
ACCESSION	AR063363					
VERSION	AR063363.1	GI:5992671				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 27)					
AUTHORS	Maertens,G., Stuyver,L., Rossau,R. and Van Heuverswyn,H.					
TITLE	Process for typing of HCV isolates					
JOURNAL	Patent: US 5846704-A 1 08-DEC-1998;					
FEATURES	Location/Qualifiers					
source	1..27					
	/organism="unknown"					
	/mol_type="unassigned DNA"					
ORIGIN						
Query Match	98.1%;	Score 20.6;	DB 6;	Length 27;		
Best Local Similarity	100.0%;	Pred. No. 4.9;				
Matches	21;	Conservative	0;	Mismatches	0;	
			Indels	0;	Gaps	0;
QY	1	CCCTGTGAGGAAGTCTGTCT 21				
Db	1	CCCTGTGAGGAAGTCTGTCT 21				
RESULT 10						
LOCUS	AR123554	27 bp	DNA	linear	PAT 16-MAY-2001	
DEFINITION	Sequence 1 from patent US 6171784.					
ACCESSION	AR123554					
VERSION	AR123554.1	GI:14108915				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 27)					
AUTHORS	Maertens,G., Stuyver,L., Rossau,R. and Van Heuverswyn,H.					
TITLE	Process for typing of HCV isolates					
JOURNAL	Patent: US 6171784-A 1 09-JAN-2001;					
FEATURES	Location/Qualifiers					
source	1..27					
	/organism="unknown"					
	/mol_type="unassigned DNA"					
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Matches	21;	Conservative	0;	Mismatches	0;	
			Indels	0;	Gaps	0;
QY	1	CCCTGTGAGGAAGTCTGTCT 21				
Db	1	CCCTGTGAGGAAGTCTGTCT 21				
RESULT 11						
LOCUS	AR267295	27 bp	DNA	linear	PAT 10-APR-2003	
DEFINITION	Sequence 1 from patent US 6495670.					
ACCESSION	AR267295					
VERSION	AR267295.1	GI:29697313				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 27)					
AUTHORS	Maertens,G., Stuyver,L., Rossau,R. and Van Heuverswyn,H.					
TITLE	Process for typing of HCV isolates					
JOURNAL	Patent: US 6495670-A 1 03-MAY-2005;					
FEATURES	Location/Qualifiers					
source	1..27					
	/organism="unknown"					
	/mol_type="unassigned DNA"					
ORIGIN						
Query Match	98.1%;	Score 20.6;	DB 6;	Length 27;		
Best Local Similarity	100.0%;	Pred. No. 4.9;				
Matches	21;	Conservative	0;	Mismatches	0;	
			Indels	0;	Gaps	0;
QY	1	CCCTGTGAGGAAGTCTGTCT 21				
Db	1	CCCTGTGAGGAAGTCTGTCT 21				
RESULT 12						
LOCUS	AR305705	27 bp	DNA	linear	PAT 12-JUN-2003	
DEFINITION	Sequence 1 from patent US 6548244.					
ACCESSION	AR305705					
VERSION	AR305705.1	GI:31695314				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 27)					
AUTHORS	Maertens,G., Stuyver,L., Rossau,R. and Van Heuverswyn,H.					
TITLE	Process for typing HCV isolates					
JOURNAL	Patent: US 6548244-A 1 15-APR-2003;					
FEATURES	Location/Qualifiers					
source	1..27					
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	/mol_type="genomic DNA"					
ORIGIN						
Query Match	98.1%;	Score 20.6;	DB 6;	Length 27;		
Best Local Similarity	100.0%;	Pred. No. 4.9;				
Matches	21;	Conservative	0;	Mismatches	0;	
			Indels	0;	Gaps	0;
QY	1	CCCTGTGAGGAAGTCTGTCT 21				
Db	1	CCCTGTGAGGAAGTCTGTCT 21				
RESULT 13						
LOCUS	AR654197	27 bp	DNA	linear	PAT 13-JUN-2005	
DEFINITION	Sequence 1 from patent US 6887985.					
ACCESSION	AR654197					
VERSION	AR654197.1	GI:67585157				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 27)					
AUTHORS	Maertens,G., Stuyver,L., Rossau,R. and Van Heuverswyn,H.					
TITLE	Process for typing of HCV isolates					
JOURNAL	Patent: US 6887985-A 1 03-MAY-2005;					
FEATURES	Location/Qualifiers					
source	1..27					
	/organism="unknown"					
	/mol_type="genomic DNA"					
ORIGIN						
Query Match	98.1%;	Score 20.6;	DB 6;	Length 27;		
Best Local Similarity	100.0%;	Pred. No. 4.9;				
Matches	21;	Conservative	0;	Mismatches	0;	
			Indels	0;	Gaps	0;
QY	1	CCCTGTGAGGAAGTCTGTCT 21				
Db	1	CCCTGTGAGGAAGTCTGTCT 21				

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source 1..27
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 98.1%; Score 20.6; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
|||||
Db 1 CCTGTGAGGAAGTCTGTCT 21

RESULT 14
AX398128 27 bp DNA linear PAT 13-JUN-2005
LOCUS
DEFINITION Sequence 1 from patent US 6891026.
ACCESSION AR655174
VERSION AR655174.1 GI:67586961
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS Maertens,G., Stuyver,L., Rossau,R. and Van Heuverswyn,H.
TITLE Process for typing of HCV isolates
JOURNAL Patent: US 6891026-A 1 10-MAY-2005;
Innogenetics N.V.; Ghent;
EPX;
FEATURES
source Location/Qualifiers
1..27
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 98.1%; Score 20.6; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
|||||
Db 1 CCTGTGAGGAAGTCTGTCT 21

RESULT 15
AX023091 27 bp DNA linear PAT 20-SEP-2000
LOCUS
DEFINITION Sequence 1 from Patent EP0905258.
ACCESSION AX023091
VERSION AX023091.1 GI:10046556
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
REFERENCE 1
AUTHORS Maertens,G., Stuyver,L., Rossau,R., Stuyver,L. and van Heuverswyn,H.
TITLE Detection and typing of hcv using 5'utr and ns5 nucleic acid
JOURNAL Patent: EP 1197568-A 1 17-APR-2002;
Innogenetics N.V. (BE)
FEATURES
source Location/Qualifiers
1..27
/organism="Hepatitis C virus"
/mol_type="unassigned DNA"
/isolate="HCV (KATO ET AL., 1992)"
/db_xref="taxon:11103"
/map="POSITION -299 OF 5' END"
misc_feature 1..27
/standard_name="UNIVERSAL HCV PRIMER HCP98"

ORIGIN
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Query Match 98.1%; Score 20.6; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
|||||
Db 1 CCTGTGAGGAAGTCTGTCT 21

RESULT 16
AX398128 27 bp DNA linear PAT 27-MAY-2002
LOCUS
DEFINITION Sequence 5 from Patent WO220837.
ACCESSION AX398128
VERSION AX398128.1 GI:21260943
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Ronaghi,M., Ekstroem,B. and Pourmand,N.
TITLE Method
JOURNAL Patent: WO 0220837-A 5 14-MAR-2002;
Pyrosequencing AB (SE) ; The Board of Trustees of The Leland
Stanford Junior University (US)
LOCATION/Qualifiers
1..27
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Oligonucleotide HCV-PCR-OUTF"

ORIGIN
Query Match 98.1%; Score 20.6; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
|||||
Db 1 CCTGTGAGGAAGTCTGTCT 21

RESULT 17
AX417297 27 bp DNA linear PAT 18-JUN-2002
LOCUS
DEFINITION Sequence 1 from Patent EP197568.
ACCESSION AX417297
VERSION AX417297.1 GI:21522601
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
REFERENCE 1
AUTHORS Maertens,G., Rossau,R., Stuyver,L. and van Heuverswyn,H.
TITLE Detection and typing of hcv using 5'utr and ns5 nucleic acid
JOURNAL Patent: EP 1197568-A 1 17-APR-2002;
Innogenetics N.V. (BE)
FEATURES
source Location/Qualifiers
1..27
/organism="Hepatitis C virus"
/mol_type="unassigned DNA"
/db_xref="taxon:11103"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21
|||||
Db 1 CCTGTGAGGAAGTCTGTCT 21
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ORIGIN

Query Match 98.1%; Score 20.6; DB 6; Length 45;  
Best Local Similarity 95.2%; Pred. No. 4.8;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21  
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Db 31 CCCTGTGAGGAAGTCTGTCT 11

RESULT 22  
BD083958/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BD083958 45 bp DNA linear PAT 27-AUG-2002  
Nucleic acid amplification method: Hybridization signal  
amplification method (HSAM).  
BD083958  
BD083958.1 GI:22629568  
JP 2001521373-A/22.  
unidentified  
unclassified.  
1 (bases 1 to 45)  
Zhang,D.Y. and Brandwein,M.  
Nucleic acid amplification method: Hybridization signal  
amplification method (HSAM)  
Patent: JP 2001521373-A 22 06-NOV-2001;  
DAVID Y ZHANG,MARGARET BRANDWEIN  
OS Unidentified  
PN JP 2001521373-A/22  
PD 06-NOV-2001  
PF 30-JUL-1997 JP 1998509121  
PR 31-JUL-1996 US 08/690495  
PI DAVID Y ZHANG,MARGARET BRANDWEIN  
PC C12Q1/68,C12Q1/70,C12P19/34,C07H21/02,C07H21/04 CC  
Strandedness: Single;  
CC Topology: Linear;  
CC Nucleic acid amplification method: Hybridization signal CC  
amplification  
CC method (HSAM)  
FH Key Location/Qualifiers  
FT source 1..45  
FT Location/Qualifiers  
1..45  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"

ORIGIN

Query Match 98.1%; Score 20.6; DB 6; Length 45;  
Best Local Similarity 95.2%; Pred. No. 4.8;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21  
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Db 31 CCCTGTGAGGAAGTCTGTCT 11

RESULT 23  
AR338407/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE

AR338407 45 bp DNA linear PAT 17-AUG-2003  
Sequence 22 from patent US 6569647.  
AR338407  
AR338407.1 GI:33725179  
Unkown.  
Unknown.  
1 (bases 1 to 45)  
Zhang,D.Y., Brandwein,M. and Hsuih,T.C.H.  
Nucleic acid amplification method: ramification-extension  
amplification method (RAM)

ORIGIN

Query Match 98.1%; Score 20.6; DB 6; Length 45;  
Best Local Similarity 95.2%; Pred. No. 4.8;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21  
|||||:|||||:|||||  
Db 31 CCCTGTGAGGAAGTCTGTCT 11

RESULT 24  
AR353602/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

AR353602 45 bp DNA linear PAT 17-AUG-2003  
Sequence 22 from patent US 6593086.  
AR353602  
AR353602.1 GI:33759633  
Unknown.  
Unknown.  
1 (bases 1 to 45)  
Zhang,D.Y.  
Nucleic acid amplification methods  
Patent: US 6593086-A 22 15-JUL-2003;  
Mount Sinai School of Medicine of New York University; New York, NY.  
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/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 98.1%; Score 20.6; DB 6; Length 45;  
Best Local Similarity 95.2%; Pred. No. 4.8;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21  
|||||:|||||:|||||  
Db 31 CCCTGTGAGGAAGTCTGTCT 11

RESULT 25  
AR636812/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

AR636812 45 bp DNA linear PAT 20-APR-2005  
Sequence 22 from patent US 6855523.  
AR636812  
AR636812.1 GI:62769941  
Unknown.  
Unknown.  
1 (bases 1 to 45)  
Zhang,D.Y., Brandwein,M. and Hsuih,T.C.H.  
Nucleic acid amplification method: ramification-extension  
amplification method (RAM)  
Patent: US 6855523-A 22 15-FEB-2005;  
Mount Sinai School of Medicine of New York University; New York, NY.  
1..45  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 98.1%; Score 20.6; DB 6; Length 45;  
Best Local Similarity 95.2%; Pred. No. 4.8;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21  
|||||:|||||:|||||  
Db 31 CCCTGTGAGGAAGTCTGTCT 11

RESULT 26  
AR636812/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

AR636812 45 bp DNA linear PAT 20-APR-2005  
Sequence 22 from patent US 6855523.  
AR636812  
AR636812.1 GI:62769941  
Unknown.  
Unknown.  
1 (bases 1 to 45)  
Zhang,D.Y., Brandwein,M. and Hsuih,T.C.H.  
Nucleic acid amplification method: ramification-extension  
amplification method (RAM)  
Patent: US 6855523-A 22 15-FEB-2005;  
Mount Sinai School of Medicine of New York University; New York, NY.  
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/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 98.1%; Score 20.6; DB 6; Length 45;  
Best Local Similarity 95.2%; Pred. No. 4.8;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTGTGAGGAAGTCTGTCT 21  
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Db 31 CCCTGTGAGGAAGTCTGTCT 11

RESULT 27  
AR636812/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE

AR636812 45 bp DNA linear PAT 17-AUG-2003  
Sequence 22 from patent US 6569647.  
AR636812  
AR636812.1 GI:33725179  
Unkown.  
Unknown.  
1 (bases 1 to 45)  
Zhang,D.Y., Brandwein,M. and Hsuih,T.C.H.  
Nucleic acid amplification method: ramification-extension  
amplification method (RAM)

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QY 1 CCTGTGAGGAACACTWCTGTCT 21
Db 31 CCTGTGAGGAACACTGTCT 11

RESULT 26
I73300 LOCUS linear PAT 03-APR-1998
DEFINITION Sequence 31 from patent US 5686272.
ACCESSION I73300
VERSION I73300.1 GI:3009439
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 51)
AUTHORS Marshall,R.L., Carrino,J.J. and Sustachek,J.C.
TITLE Amplification of RNA sequences using the ligase chain reaction
JOURNAL Patent: US 5686272-A 31 11-NOV-1997;
FEATURES
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    1..51
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    /mol_type="unassigned DNA"
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Query Match 98.1%; Score 20.6; DB 6; Length 51;
Best Local Similarity 95.2%; Pred. No. 4.7;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAACACTWCTGTCT 21
Db 16 CCTGTGAGGAACACTGTCT 36

RESULT 27
AR095004/c LOCUS linear PAT 08-SEP-2000
DEFINITION Sequence 42 from patent US 6001990.
ACCESSION AR095004
VERSION AR095004.1 GI:10022461
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 67)
AUTHORS Wands,J.R., Wakita,T. and Moradpour,D.
TITLE Antisense inhibition of hepatitis C virus
JOURNAL Patent: US 6001990-A 42 14-DEC-1999;
FEATURES
    Location/Qualifiers
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    /organism="unknown"
    /mol_type="unassigned DNA"
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Query Match 98.1%; Score 20.6; DB 6; Length 67;
Best Local Similarity 95.2%; Pred. No. 4.7;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAACACTWCTGTCT 21
Db 25 CCTGTGAGGAACACTGTCT 5

RESULT 28
BD171247 LOCUS linear PAT 17-JAN-2003
DEFINITION Method of detecting pathogenic microorganism.
ACCESSION BD171247
VERSION BD171247.1 GI:27877059
KEYWORDS WO 02052043-A/39,
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 73)
AUTHORS Shimada,M., Hino,F. and Kato,I.
TITLE Method of detecting pathogenic microorganism
JOURNAL Patent: WO 02052043-A 39 04-JUL-2002;
COMMENT TAKARA SHUZO CO LTD,MASAMITSU SHIMADA,FUMITSUGU HINO,IKUNOSHIN KATO
OS Artificial Sequence
PN WO 02052043-A/39
PD 04-JUL-2002
PF 26-DEC-2001 WO 2001JP011422
PR 26-DEC-2000 JP OOP 396222,26-DEC-2000 JP OOP 396321 PR
29-JUN-2001 JP O1P 199552,13-SEP-2001 JP O1P 278920 PI
MASAMITSU SHIMADA,FUMITSUGU HINO,IKUNOSHIN KATO PC
C12Q1/68,C12N15/09
CC Primer area to amplify a portion of HCV.
FH Key Location/Qualifiers
FT source 1..73
/organism='Artificial Sequence'.
FEATURES
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    /mol_type="genomic DNA"
    /db_xref="taxon:32630"
ORIGIN
Query Match 98.1%; Score 20.6; DB 6; Length 73;
Best Local Similarity 95.2%; Pred. No. 4.6;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAACACTWCTGTCT 21
Db 21 CCTGTGAGGAACACTGTCT 41

RESULT 29
CQ830528 LOCUS linear PAT 12-JUL-2004
DEFINITION Sequence 2 from Patent WO2004055210.
ACCESSION CQ830528
VERSION CQ830528.1 GI:50250861
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Balakireva,I.
TITLE Molecules inhibiting hepatitis c virus protein synthesis and method
for screening same
JOURNAL Patent: WO 2004055210-A 2 01-JUL-2004;
UNIVERSITE JOSEPH FOURIER (FR)
FEATURES
    Location/Qualifiers
    1..80
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    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="R gion II de l'RES de VHC"
ORIGIN
Query Match 98.1%; Score 20.6; DB 6; Length 80;
Best Local Similarity 95.2%; Pred. No. 4.6;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAACACTWCTGTCT 21
Db 4 CCTGTGAGGAACACTGTCT 24

RESULT 30
CS001589 LOCUS linear VRL 01-FEB-2005
DEFINITION Sequence 5 from Patent WO2005005625.
ACCESSION CS001589
VERSION CS001589
KEYWORDS CS001589.1 GI:58424011

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SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.

REFERENCE 1  
AUTHORS Sonenberg,N. and Lopez Lastra,M.  
TITLE Method for inducing hepatitis c virus (hcv) replication in vitro,  
cells and cell lines enabling robust hcv replication and kit  
therefor

JOURNAL Patent: WO 2005005625-A 20-JAN-2005;  
McGill University (CA)  
FEATURES source  
Location/Qualifiers  
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/organism="Hepatitis C virus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:11103"

ORIGIN  
Query Match 98.1%; Score 20.6; DB 13; Length 131;  
Best Local Similarity 95.2%; Pred. No. 4.5;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21  
Db 6 CCTGTGAGGAAGTCTGTCT 26

RESULT 31  
CS001590  
LOCUS 131 bp DNA linear VRL 01-FEB-2005  
DEFINITION Sequence 6 from Patent WO2005005625.  
ACCESSION CS001590  
VERSION CS001590.1 GI:58424012  
KEYWORDS  
SOURCE Cercopithecine herpesvirus 15 (Rhesus lymphocryptovirus)  
ORGANISM Cercopithecine herpesvirus 15  
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
Gammaherpesvirinae; Lymphocryptovirus.

REFERENCE 1  
AUTHORS Sonenberg,N. and Lopez Lastra,M.  
TITLE Method for inducing hepatitis c virus (hcv) replication in vitro,  
cells and cell lines enabling robust hcv replication and kit  
therefor

JOURNAL Patent: WO 2005005625-A 20-JAN-2005;  
McGill University (CA)  
FEATURES source  
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Query Match 98.1%; Score 20.6; DB 13; Length 131;  
Best Local Similarity 95.2%; Pred. No. 4.5;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21  
Db 6 CCTGTGAGGAAGTCTGTCT 26

RESULT 32  
CS001591  
LOCUS 131 bp DNA linear VRL 01-FEB-2005  
DEFINITION Sequence 7 from Patent WO2005005625.  
ACCESSION CS001591  
VERSION CS001591.1 GI:58424013  
KEYWORDS  
SOURCE Cercopithecine herpesvirus 15 (Rhesus lymphocryptovirus)  
ORGANISM Cercopithecine herpesvirus 15  
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
Gammaherpesvirinae; Lymphocryptovirus.

REFERENCE 1

AUTHORS Sonenberg,N. and Lopez Lastra,M.  
TITLE Method for inducing hepatitis c virus (hcv) replication in vitro,  
cells and cell lines enabling robust hcv replication and kit  
therefor

JOURNAL Patent: WO 2005005625-A 20-JAN-2005;  
McGill University (CA)  
FEATURES source  
Location/Qualifiers  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:45455"

ORIGIN  
Query Match 98.1%; Score 20.6; DB 13; Length 131;  
Best Local Similarity 95.2%; Pred. No. 4.5;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21  
Db 6 CCTGTGAGGAAGTCTGTCT 26

RESULT 33  
CS001592  
LOCUS 131 bp DNA linear VRL 01-FEB-2005  
DEFINITION Sequence 8 from Patent WO2005005625.  
ACCESSION CS001592  
VERSION CS001592.1 GI:58424014  
KEYWORDS  
SOURCE Cercopithecine herpesvirus 15 (Rhesus lymphocryptovirus)  
ORGANISM Cercopithecine herpesvirus 15  
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
Gammaherpesvirinae; Lymphocryptovirus.

REFERENCE 1  
AUTHORS Sonenberg,N. and Lopez Lastra,M.  
TITLE Method for inducing hepatitis c virus (hcv) replication in vitro,  
cells and cell lines enabling robust hcv replication and kit  
therefor

JOURNAL Patent: WO 2005005625-A 20-JAN-2005;  
McGill University (CA)  
FEATURES source  
Location/Qualifiers  
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ORIGIN  
Query Match 98.1%; Score 20.6; DB 13; Length 131;  
Best Local Similarity 95.2%; Pred. No. 4.5;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGTGAGGAAGTCTGTCT 21  
Db 6 CCTGTGAGGAAGTCTGTCT 26

RESULT 34  
CS001593  
LOCUS 131 bp DNA linear VRL 01-FEB-2005  
DEFINITION Sequence 9 from Patent WO2005005625.  
ACCESSION CS001593  
VERSION CS001593.1 GI:58424015  
KEYWORDS  
SOURCE Cercopithecine herpesvirus 15 (Rhesus lymphocryptovirus)  
ORGANISM Cercopithecine herpesvirus 15  
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
Gammaherpesvirinae; Lymphocryptovirus.

REFERENCE 1  
AUTHORS Sonenberg,N. and Lopez Lastra,M.  
TITLE Method for inducing hepatitis c virus (hcv) replication in vitro,  
cells and cell lines enabling robust hcv replication and kit  
therefor

JOURNAL Patent: WO 2005005625-A 20-JAN-2005;

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QY		1 CCTGTGAGGAAGTCTGTCT 21 		1 CCCTGTGAGGAAGTCTGTCT 21 	
Db		6 CCCTGTGAGGAAGTCTGTCT 26 		113 CCCTGTGAGGAAGTCTGTCT 93 	
RESULT 35		CS001594 131 bp DNA linear VRL 01-FEB-2005		AF506627 232 bp RNA linear VRL 20-MAY-2002	
LOCUS		Sequence 10 from Patent WO2005005625.		Hepatitis C virus isolate RIG101 5' untranslated region, partial	
ACCESSION		CS001594		AF506627	
VERSION		CS001594.1 GI:58424016		AF506627.1 GI:20977971	
KEYWORDS		Cercopithecine herpesvirus 15 (Rhesus lymphocryptovirus)		Hepatitis C virus	
SOURCE		Cercopithecine herpesvirus 15		Hepatitis C virus	
ORGANISM		Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Lymphocryptovirus.		Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.	
REFERENCE		1 Sonenberg,N. and Lopez Lastra,M. Method for inducing hepatitis c virus (hcv) replication in vitro, cells and cell lines enabling robust hcv replication and kit therefor Patent: WO 2005005625-A 20-JAN-2005; McGill University (CA)		1 (bases 1 to 232) Shustov,A.V., Gavrilova,I.V. and Netesov,S.V. Genetic variability of hepatitis C virus in Western Siberia Unpublished 2 (bases 1 to 232) Shustov,A.V., Gavrilova,I.V. and Netesov,S.V. Direct Submission Submitted (26-APR-2002) Inst. Molecular Biology, State Research Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl. 630559, Russia	
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Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;		Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;		Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY		1 CCCTGTGAGGAAGTCTGTCT 21 		1 CCCTGTGAGGAAGTCTGTCT 21 	
Db		6 CCCTGTGAGGAAGTCTGTCT 26 		3 CCCTGTGAGGAAGTCTGTCT 23 	
RESULT 36		AR095003 155 bp DNA linear PAT 08-SEP-2000		AF506629 232 bp RNA linear VRL 20-MAY-2002	
LOCUS		Sequence 41 from patent US 6001990.		Hepatitis C virus isolate KGV126 5' untranslated region, partial	
ACCESSION		AR095003		AF506629	
VERSION		AR095003.1 GI:10022459		AF506629.1 GI:20977973	
KEYWORDS		Unknown.		Hepatitis C virus	
SOURCE		Unknown.		Hepatitis C virus	
ORGANISM		Unclassified.		Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.	
REFERENCE		1 (bases 1 to 155) Wands,J.R., Wakita,T. and Moradpour,D. Antisense inhibition of hepatitis C virus Patent: US 6001990-A 41 14-DEC-1999;		1 (bases 1 to 232) Shustov,A.V., Gavrilova,I.V. and Netesov,S.V. Genetic variability of hepatitis C virus in Western Siberia Unpublished 2 (bases 1 to 232) Shustov,A.V., Gavrilova,I.V. and Netesov,S.V. Direct Submission Submitted (26-APR-2002) Inst. Molecular Biology, State Research Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl. 630559, Russia	
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ORIGIN		Query Match 98.1%; Score 20.6; DB 6; Length 155; Best Local Similarity 95.2%; Pred. No. 4.4;			

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Best Local Similarity 95.2%; Pred. No. 4.3;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAAGTCTGTCT 21
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Db 4 CCCTGTGAGGAAGTCTGTCT 24

RESULT 39
AF506666      232 bp RNA linear VRL 20-MAY-2002
LOCUS Hepatitis C virus isolate KMA22 5' untranslated region, partial
DEFINITION
ACCESSION AF506666
VERSION AF506666
KEYWORDS
SOURCE
ORGANISM Hepatitis C virus
Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE 1 (bases 1 to 232)
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.
TITLE Genetic variability of hepatitis C virus in Western Siberia
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 232)
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.
TITLE Direct Submission
JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research
Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl.
630559, Russia
LOCATION/Qualifiers
1..232
/organism="Hepatitis C virus"
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/isoate="KGV58"
/db_xref="taxon:11103"
/country="Russia"
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5'UTR
ORIGIN

Query Match      98.1%; Score 20.6; DB 13; Length 232;
Best Local Similarity 95.2%; Pred. No. 4.3;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAAGTCTGTCT 21
    |||||:|||||:|||||
Db 3 CCCTGTGAGGAAGTCTGTCT 23

RESULT 41
BD182732      238 bp DNA linear PAT 17-JUN-2003
LOCUS Profile database and method for preparing profile.
DEFINITION
ACCESSION BD182732.1 GI:31874932
VERSION JP 2002358309-A/2.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 238)
AUTHORS Yatsuka,S., Muto,I., Yamashita,I. and Tamura,T.
TITLE Profile database and method for preparing profile
JOURNAL Patent: JP 2002358309-A 2 13-DEC-2002;
COMMENT HITACHI SOFTWARE ENGINEERING CO LTD
OS Homo sapiens (human)
PN JP 2002358309-A/2
PD 13-DEC-2002
PF 04-JUN-2001 JP 2001168230
PI SHIGERU YATSUKA, ISAMU MUTO, IWAO YAMASHITA, TAKURO TAMURA PC
G06F17/30//C12N15/09,C12Q1/68,C12N15/00
CC Profile database and method for preparing profile FH Key
LOCATION/Qualifiers
1..238
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FEATURES
source
1..238
/organism="Homo sapiens"
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ORIGIN

Query Match      98.1%; Score 20.6; DB 6; Length 238;
Best Local Similarity 95.2%; Pred. No. 4.3;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAAGTCTGTCT 21
    |||||:|||||:|||||
Db 43 CCCTGTGAGGAAGTCTGTCT 63

RESULT 42
BD182733      238 bp DNA linear PAT 17-JUN-2003
LOCUS Profile database and method for preparing profile.
DEFINITION
ACCESSION BD182733
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VERSION	BD182733.1	GI:31874933
KEYWORDS	JP 2002358309-A/3.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 238)	
AUTHORS	Yatsuka,S., Muto,I., Yamashita,I. and Tamura,T.	
TITLE	Profile database and method for preparing profile	
JOURNAL	Patient: JP 2002358309-A 3 13-DEC-2002;	
COMMENT	HITACHI SOFTWARE ENGINEERING CO LTD	
	OS Homo sapiens (human)	
	PN JP 2002358309-A/3	
	PD 13-DEC-2002	
	PF 04-JUN-2001 JP 2001168230	
	PI SHIGERU YATSUKA, ISAMU MUTO, IWAO YAMASHITA, TAKURO TAMURA PC	
	G06F17/30//C12N15/09,C12Q1/68,C12N15/00	
	CC Profile database and method for preparing profile FH Key	
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FEATURES	Location/Qualifiers	/organism='Homo sapiens (human)'. 1..238
ORIGIN		
Query Match	98.1%; Score 20.6; DB 6; Length 238;	
Best Local Similarity	95.2%; Pred. No. 4.3;	
Matches	20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 CCCTGTGAGGAACACTGCTGCT 21 	
Dd	43 CCCTGTGAGGAACACTGCTGCT 63 	
RESULT 43		
BD182735		
LOCUS	BD182735	238 bp DNA linear PAT 17-JUN-2003
DEFINITION	Profile database and method for preparing profile.	
ACCESSION	BD182735	
VERSION	BD182735.1	GI:31874935
KEYWORDS	JP 2002358309-A/5.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 238)	
AUTHORS	Yatsuka,S., Muto,I., Yamashita,I. and Tamura,T.	
TITLE	Profile database and method for preparing profile	
JOURNAL	Patient: JP 2002358309-A 5 13-DEC-2002;	
COMMENT	HITACHI SOFTWARE ENGINEERING CO LTD	
	OS Homo sapiens (human)	
	PN JP 2002358309-A/5	
	PD 13-DEC-2002	
	PF 04-JUN-2001 JP 2001168230	
	PI SHIGERU YATSUKA, ISAMU MUTO, IWAO YAMASHITA, TAKURO TAMURA PC	
	G06F17/30//C12N15/09,C12Q1/68,C12N15/00	
	CC Profile database and method for preparing profile FH Key	
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ORIGIN		
Query Match	98.1%; Score 20.6; DB 6; Length 238;	

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/organism="Hepatitis C virus"
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Best Local Similarity 95.2%; Pred. No. 4.3;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAACCTWCTGTCT 21
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Db 3 CCCTGTGAGGAACCTTCTGTCT 23

RESULT 46
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LOCUS      239 bp      DNA      linear      PAT 17-JUN-2003
DEFINITION Profile database and method for preparing profile.
ACCESSION  BD182734
VERSION    BD182734.1 GI:31874934
KEYWORDS  JP 2002358309-A/4.
SOURCE    Homo sapiens (human)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homidae; Homo
          1 (bases 1 to 239)
REFERENCE  Yatsuka,S., Muto,I., Yamashita,I. and Tamura,T.
          TITLE Profile database and method for preparing profile
          JOURNAL Patent: JP 2002358309-A 4 13-DEC-2002;
          HITACHI SOFTWARE ENGINEERING CO LTD
          OS Homo sapiens (human)
          PN JP 2002358309-A/4
          PD 13-DEC-2002
          PI 04-JUN-2001 JP 2001168230
          PT SHIGERU YATSUKA,IGAMU MUTO,IWAO YAMASHITA,TAKURO TAMURA PC
          G06F17/30//C12N15/09,C12Q1/68,C12N15/00
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FEATURES
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Query Match      98.1%; Score 20.6; DB 6; Length 239;
Best Local Similarity 95.2%; Pred. No. 4.3;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAACCTWCTGTCT 21
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Db 43 CCCTGTGAGGAACCTACTGTCT 63

RESULT 47
AF506683
LOCUS      239 bp      RNA      linear      VRL 20-MAY-2002
DEFINITION Hepatitis C virus isolate KGV54 5' untranslated region, partial
sequence.
ACCESSION  AF506683
VERSION    AF506683.1 GI:20978027
KEYWORDS  Hepatitis C virus
SOURCE    Hepatitis C virus
ORGANISM  Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
          Hepacivirus.
          1 (bases 1 to 239)
REFERENCE  1
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AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.
TITLE   Genetic variability of hepatitis C virus in Western Siberia
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 239)
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.
TITLE   Direct Submission
JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research
Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl.
630559, Russia
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Query Match      98.1%; Score 20.6; DB 13; Length 239;
Best Local Similarity 95.2%; Pred. No. 4.3;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAACCTWCTGTCT 21
    |||||
Db 3 CCCTGTGAGGAACCTTCTGTCT 23

RESULT 48
AF506687
LOCUS      242 bp      RNA      linear      VRL 20-MAY-2002
DEFINITION Hepatitis C virus isolate KMA3 5' untranslated region, partial
sequence.
ACCESSION  AF506687
VERSION    AF506687.1 GI:20978031
KEYWORDS  Hepatitis C virus
SOURCE    Hepatitis C virus
ORGANISM  Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
          Hepacivirus.
          1 (bases 1 to 242)
REFERENCE  Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.
          TITLE Genetic variability of hepatitis C virus in Western Siberia
          JOURNAL Unpublished
          REFERENCE 2 (bases 1 to 242)
          AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.
          TITLE Direct Submission
          JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research
Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl.
630559, Russia
FEATURES Location/Qualifiers
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/db_xref="taxon:11103"
/country="Russia"
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5'UTR
ORIGIN
Query Match      98.1%; Score 20.6; DB 13; Length 242;
Best Local Similarity 95.2%; Pred. No. 4.3;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGTGAGGAACCTWCTGTCT 21
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Db 4 CCCTGTGAGGAACCTTCTGTCT 24

RESULT 49
AY344040
LOCUS      258 bp      RNA      linear      VRL 23-APR-2004
DEFINITION Hepatitis C virus isolate UT-S44 5' UTR.
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ACCESSION AY344040  
VERSION AY344040.1 GI:37790679  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.  
REFERENCE 1 (bases 1 to 258)  
AUTHORS Bhattacharyya,S., Mapa,K., Prabhavathi,S., Sudhamani,S.R., Menon,P.K., John,K.P., Shivaram,C., Amarnath,S. and Das,S.  
TITLE Phylogenetic conservation of the stem-loop III structure of the 5'untranslated region of Hepatitis C virus RNA among natural variants in samples collected from Southern India  
JOURNAL Arch. Virol. 149 (5), 1015-1026 (2004)  
PUBMED 15098115  
REFERENCE 2 (bases 1 to 258)  
AUTHORS Bhattacharyya,S., Prabhavathi,S., Mapa,K. and Das,S.  
TITLE Direct Submission  
JOURNAL Submitted (16-JUL-2003) Microbiology & Cell Biology, Indian Institute of Science, C.V. Raman Street, Bangalore, Karnataka 560012, India  
FEATURES  
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Query Match 98.1%; Score 20.6; DB 13; Length 258;  
Best Local Similarity 95.2%; Pred. No. 4.3;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
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Db 21 CCCTGTGAGGAAGTCTGTCT 41  
RESULT 50  
AR095002/c 260 bp DNA linear PAT 08-SEP-2000  
LOCUS  
DEFINITION Sequence 40 from patent US 6001990.  
ACCESSION AR095002  
VERSION AR095002.1 GI:10022457  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 260)  
AUTHORS Wands,J.R., Wakita,T. and Moradpour,D.  
TITLE Antisense inhibition of hepatitis C virus  
JOURNAL Patent: US 6001990-A 40 14-DEC-1999;  
FEATURES  
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Best Local Similarity 95.2%; Pred. No. 4.3;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CCCTGTGAGGAAGTCTGTCT 21  
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Db 218 CCCTGTGAGGAAGTCTGTCT 198

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Maximum Match 100%  
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12: geneseqn2004as.\*  
13: geneseqn2004bs.\*  
14: geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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3	20	95.2	581	10	ABX08685 Pathogeni
4	20	95.2	581	10	ABX08683 Pathogeni
5	20	95.2	581	10	ABX08684 Pathogeni
6	20	95.2	581	12	ADL92264 Human MxA
7	19.4	92.4	46	12	ADL92256 Human MxA
8	19.4	92.4	132	12	ADO78057 Human MxA
9	19.4	92.4	132	12	ADO78056 Human MxA
10	19.4	92.4	581	4	AAI70373 Human MxA
11	19.4	92.4	581	4	AAI70375 Human MxA
12	19.4	92.4	581	4	AAI70376 Human MxA
13	19.4	92.4	581	4	AAI70374 Human MxA
14	19.4	92.4	581	5	AAI70353 Promoter
15	19.4	92.4	581	5	AAI70350 Promoter
16	19.4	92.4	581	5	AAI70352 Promoter
17	19.4	92.4	581	5	AAI70351 Promoter
18	19.4	92.4	581	10	ABX08706 Pathogeni
19	19.4	92.4	581	10	ABX08704 Pathogeni

20	19.4	92.4	581	10	ABX08705
21	19.4	92.4	581	12	ADL92270 Human MxA
22	19.4	92.4	581	12	ADL92267 Human MxA
23	19.4	92.4	2451	9	AAI55593 Human MxA
24	19.4	92.4	5376	9	AAI55595 Luciferas
25	19.4	92.4	49343	14	ABE96544 Human MX1
26	18.4	87.6	581	12	ADL92263 Human MxA
27	18.4	87.6	581	12	ADL92266 Human MxA
28	18.4	87.6	581	12	ADL92265 Human MxA
29	17.8	84.8	581	12	ADL92269 Human MxA
30	17.8	84.8	581	12	ADL92268 Human MxA
31	17.8	84.8	581	6	ABL34192 Human imm
32	17.8	84.8	581	6	ABL70483 Chemical
33	17	81.0	3302	6	ABL69125 Kidney ca
34	17	81.0	3302	13	ADR14356 Human NF-
35	17	81.0	3302	14	ADX07310 Cyclin-de
36	17	81.0	3302	14	ADZ49006 Insulin s
37	17	81.0	3302	14	ABE56452 Radiochem
38	17	81.0	3579	11	ACN90319 Breast ca
39	16.8	80.0	633	8	ACF74962 Staphyloc
40	16.8	80.0	954	5	AAI593751 DNA encod
41	16.8	80.0	1840	5	AAI581868 DNA encod
42	16.8	80.0	1972	3	AAI01353 Wheat sph
43	16.8	80.0	2178	5	AAI581864 DNA encod
44	16.8	80.0	2179	5	AAI589697 DNA encod
45	16.8	80.0	2250	5	AAI593754 DNA encod
46	16.8	80.0	2830	5	AAI593758 DNA encod
47	16.8	80.0	3039	5	AAI593339 DNA encod
48	16.8	80.0	3039	5	AAI589661 DNA encod
49	16.8	80.0	3039	5	AAI593240 DNA encod
50	16.8	80.0	3355	4	AAI585756 DNA encod
51	16.8	80.0	4134	4	AAI582650 E. coli D
52	16.8	80.0	4134	4	AAI584668 E. coli g
53	16.8	80.0	4134	8	AAI18677 Prokaryot
54	16.8	80.0	4194	8	AAI19005 Prokaryot
55	16.8	80.0	4236	8	AAI19006 Prokaryot
56	16.8	80.0	5471	5	AAI590210 DNA encod
57	16.8	80.0	5519	9	ACD19213 E. coli 0
58	16.8	80.0	5526	10	ADC01425 Enterohae
59	16.8	80.0	9072	2	AAI74356 Staphyloc
60	16.4	78.1	2216	13	ADR07421 Full leng
61	16.4	78.1	2394	12	ADQ76241 Bacillus
62	16.4	78.1	2394	12	ADQ76240 Bacillus
63	16.2	77.1	270	14	ADW83075 MAP3K9 ma
64	16.2	77.1	446	4	AAI63460 Human imm
65	16.2	77.1	647	4	AAI32234 Human olf
66	16.2	77.1	647	2	AAI32234 Human olf
67	16.2	77.1	648	2	AAI091406 Human olf
68	16.2	77.1	945	4	AAI32454 Human olf
69	16.2	77.1	945	4	AAI32461 Human olf
70	16.2	77.1	945	4	AAI31761 Human olf
71	16.2	77.1	945	12	ADG76812 Human olf
72	16.2	77.1	954	12	ACH91738 Human gen
73	16.2	77.1	989	6	ABT04154 Human G-p
74	16.2	77.1	989	12	ADH30847 Human G-p
75	16.2	77.1	995	6	ABQ88369 Human G-p
76	16.2	77.1	995	10	ADJ04274 Human G-p
77	16.2	77.1	1110	2	AAI51701 DNA encod
78	16.2	77.1	1110	6	ABQ92553 Human sec
79	16.2	77.1	1110	8	ADA40004 Human sec
80	16.2	77.1	1110	8	ACC50556 Human sec
81	16.2	77.1	1110	10	ADA56193 Gene enco
82	16.2	77.1	1146	5	AAI71758 DNA encod
83	16.2	77.1	1282	10	ACA56815 Human sig
84	16.2	77.1	1282	12	ADI56611 Human pol
85	16.2	77.1	1324	12	ADJ40698 Plant CDN
86	16.2	77.1	1481	13	ADT19956 Plant CDN
87	16.2	77.1	1668	13	ADT19956 Plant ful
88	16.2	77.1	1713	12	ADP04057 Human col
89	16.2	77.1	2000	10	ACC60728 Gene sequ
90	16.2	77.1	2000	10	ADK61825 Disease t
91	16.2	77.1	2746	13	ADT18862 Plant CDN
92	16.2	77.1	3009	13	ADS46635 Bacterial





```
Db          410 GCAAGTGTGAGTGGCGGG 430
RESULT 3
ABX08685
ID ABX08685 standard; DNA; 581 BP.
XX
AC ABX08685;
XX
DT 20-JAN-2003 (first entry)
XX
DE Pathogenic organism detection method associated DNA sequence #4.
XX
KW Gene; ss; hepatitis C virus; human; pathogenic microorganism; influenza;
KW AIDS; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200277281-A1.
XX
PD 03-OCT-2002.
XX
PF 05-MAR-2002; 2002WO-JP002030.
XX
PR 27-MAR-2001; 2001JP-00090053.
PR 18-SEP-2001; 2001JP-00284112.
XX
PA (TOKE ) TOSHIBA KK.
XX
PI Hashimoto K, Hashimoto M, Mishiro S, Oota Y;
XX
DR WPI; 2003-040593/03.
XX
PT Detecting nucleic acids relating diseases particularly due to pathogenic
PT microorganisms e.g. hepatitis, influenza and AIDS in individuals from
PT their data using immobilized probes on substrate, also for therapeutic
PT evaluation.
XX
PS Claim 15; Page 89; 125pp; Japanese.
XX
CC This invention relates to a method for obtaining first data on a nucleic
CC acid from an individual exposed to a specific disease and second data on
CC a nucleic acid from a pathogenic microorganism occurring in the
CC individual in order to relate the specific disease to such pathogenic
CC microorganism. The method of the invention comprises the reaction of a
CC nucleic acid extract from the individual with a probe-immobilization
CC substrate containing first and second probes for detection of the
CC pathogenic microorganism with the first probe to relate to the specific
CC nucleic acid in the individual and obtaining first data from the reaction
CC results as well as the detected binding of a nucleic acid with the first
CC probe and/or second data from the detected binding of a nucleic acid with
CC the second probe. The method of the invention is useful for detecting
CC nucleic acids relating diseases particularly due to pathogenic
CC microorganisms e.g. hepatitis C, influenza and AIDS in individuals, and
CC also for therapeutic evaluation. Such a method is convenient and accurate
CC and may be used to design specific therapy for effective treatment even
CC for individual patients in a tailor-made manner. The present sequence
CC represents a nucleic acid sequence used in the scope of the invention
XX
SQ Sequence 581 BP; 118 A; 148 C; 214 G; 100 T; 0 U; 1 Other;
Query Match 95.2%; Score 20; DB 10; Length 581;
Best Local Similarity 95.2%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCAAGTGTGAGTGGCGGG 21
|||||
Db 410 GCAAGTGTGAGTGGCGGG 430
RESULT 5
ABX08684
ID ABX08684 standard; DNA; 581 BP.
XX
AC ABX08684;
XX
DT 20-JAN-2003 (first entry)
XX
```

XX DE Pathogenic organism detection method associated DNA sequence #3.  
XX DE Gene; ss; hepatitis C virus; human; pathogenic microorganism; influenza;  
KW AIDS; acquired immunodeficiency syndrome.  
XX OS Homo sapiens.  
XX WO200277281-A1.  
XX PN 03-OCT-2002.  
XX PD 05-MAR-2002; 2002WO-JP002030.  
XX PF 27-MAR-2001; 2001JP-00090053.  
XX PR 18-SEP-2001; 2001JP-00284112.  
XX PA (TOKE ) TOSHIBA KK.  
XX PI Hashimoto K, Hashimoto M, Mishiro S, Oota Y;  
XX WPI; 2003-040593/03.  
XX DR  
XX PT Detecting nucleic acids relating diseases particularly due to pathogenic  
XX PT microorganisms e.g. hepatitis, influenza and AIDS in individuals from  
XX PT their data using immobilized probes on substrate, also for therapeutic  
XX PT evaluation.  
XX PS Claim 15; Page 88; 125pp; Japanese.  
XX SQ  
CC This invention relates to a method for obtaining first data on a nucleic  
CC acid from an individual exposed to a specific disease and second data on  
CC a nucleic acid from a pathogenic microorganism occurring in the  
CC individual in order to relate the specific disease to such pathogenic  
CC microorganism. The method of the invention comprises the reaction of a  
CC nucleic acid extract from the individual with a probe-immobilization  
CC substrate containing first and second probes for detection of the  
CC pathogenic microorganism with the first probe to relate to the specific  
CC microbe-caused disease, and the second probe for detecting a specific  
CC nucleic acid in the individual and obtaining first data from the reaction  
CC results as well as the detected binding of a nucleic acid with the first  
CC probe and/or second data from the detected binding of a nucleic acid with  
CC the second probe. The method of the invention is useful for detecting  
CC nucleic acids relating diseases particularly due to pathogenic  
CC microorganisms e.g. hepatitis C, influenza and AIDS in individuals, and  
CC also for therapeutic evaluation. Such a method is convenient and accurate  
CC and may be used to design specific therapy for effective treatment even  
CC for individual patients in a tailor-made manner. The present sequence  
CC represents a nucleic acid sequence used in the scope of the invention  
XX SQ Sequence 581 BP; 119 A; 147 C; 214 G; 100 T; 0 U; 1 Other;  
Query Match 95.2%; Score 20; DB 10; Length 581;  
Best Local Similarity 95.2%; Pred. No. 22;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GCAAGTCTGTAGTGGGG 21  
Db 410 GCAAGTCTGNAGTGGGG 430  
RESULT 6  
ADL92264  
ID ADL92264 standard; DNA; 581 BP.  
XX AC ADL92264;  
XX DT 20-MAY-2004 (first entry)  
XX DE Human MxA gene DNA sequence #2.  
XX KW nucleic acid detection; immobilised nucleic acid probe;  
KW single nucleotide polymorphism detection; SNP detection;  
KW  
XX

KW disease diagnosis; ds; human; MxA gene.  
XX OS Homo sapiens.  
XX PN JP2004041109-A.  
XX PD 12-FEB-2004.  
XX PF 12-JUL-2002; 2002JP-00204444.  
XX PR 12-JUL-2002; 2002JP-00204444.  
XX PA (TOKE ) TOSHIBA KK.  
XX DR WPI; 2004-151026/15.  
XX PT Detecting target nucleic acid (T) using probe, comprises amplifying  
XX PT target sequence (S) so that end of (S) which is hybridized with probe is  
XX PT positioned at less than 40 bases from terminal base of (T) and detecting  
XX PT hybridization with probe.  
XX PS Disclosure; SEQ ID NO 21; 47pp; Japanese.  
XX SQ Sequence 581 BP; 118 A; 147 C; 215 G; 100 T; 0 U; 1 Other;  
Query Match 95.2%; Score 20; DB 12; Length 581;  
Best Local Similarity 95.2%; Pred. No. 22;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GCAAGTCTGTAGTGGGG 21  
Db 410 GCAAGTCTGNAGTGGGG 430  
RESULT 7  
ADL92256  
ID ADL92256 standard; DNA; 46 BP.  
XX AC ADL92256;  
XX DT 20-MAY-2004 (first entry)  
XX DE Human MxA gene PCR primer #2.  
XX KW nucleic acid detection; immobilised nucleic acid probe;  
KW single nucleotide polymorphism detection; SNP detection;  
KW disease diagnosis; PCR; primer; ss; human; MxA gene.  
XX OS Homo sapiens.  
XX PN JP2004041109-A.  
XX PD 12-FEB-2004.  
XX PF 12-JUL-2002; 2002JP-00204444.  
XX PR 12-JUL-2002; 2002JP-00204444.  
XX PA (TOKE ) TOSHIBA KK.  
XX DR WPI; 2004-151026/15.  
XX PT Detecting target nucleic acid (T) using probe, comprises amplifying  
XX PT target sequence (S) so that end of (S) which is hybridized with probe is  
XX PT positioned at less than 40 bases from terminal base of (T) and detecting

PT hybridization with probe.  
XX  
PS Claim 6; SEQ ID NO 13; 47bp; Japanese.  
XX  
CC The invention comprises a method for detecting a target nucleic acid. The  
CC method of the invention is useful for: single nucleotide polymorphism  
CC detection, diagnosis of disease by analysing disease-related genes,  
CC estimating risk of incidence of the disease, detection of infection,  
CC analysing virus types, and in toxicity studies. The present DNA sequence  
CC represents a PCR primer of the invention.  
XX  
SQ Sequence 46 BP; 7 A; 9 C; 19 G; 11 T; 0 U; 0 Other;  
  
Query Match 92.4%; Score 19.4; DB 12; Length 46;  
Best Local Similarity 95.2%; Pred. No. 34;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GCAAGTGTCTAGGTGCGGG 21  
DB 4 GCAAGTGTCTAGGTGCGGG 24  
  
RESULT 8  
ADO78057/c  
ID ADO78057 standard; DNA; 132 BP.  
XX  
AC ADO78057;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Human MxA gene promoter region #2.  
XX  
KW nucleic acid analysis; single nucleotide polymorphism detection;  
KW SNP detection; human; MxA; promoter; ds.  
XX  
OS Homo sapiens.  
XX  
PN JP2004121044-A.  
XX  
PD 22-APR-2004.  
XX  
PF 30-SEP-2002; 2002JP-00287376.  
XX  
PR 30-SEP-2002; 2002JP-00287376.  
XX  
PA (TOKE ) TOSHIBA KK.  
XX  
DR WPI; 2004-322749/30.  
XX  
PT Analyzing nucleic acid sequence, involves allowing nucleic acid in sample  
PT to react and hybridize with first and second probe having homologous  
XX sequence except for single base at target region.  
XX  
PS Example 1; SEQ ID NO 2; 16pp; Japanese.  
XX  
CC The invention comprises a method for analysing a nucleic acid sequence,  
CC the method involves allowing the nucleic acid in a sample to hybridise  
CC with a first probe and a second probe which is shorter than the first  
CC probe by one base, where the sequence of the first and second probe are  
CC homologous except for a single base at the target region. The method of  
CC the invention is useful for analysing nucleic acid sequences (e.g. single  
CC nucleotide polymorphism detection). The present DNA sequence represents a  
CC region of the human MxA gene promoter which was used in an example of the  
CC invention.  
XX  
SQ Sequence 132 BP; 22 A; 46 C; 38 G; 26 T; 0 U; 0 Other;  
  
Query Match 92.4%; Score 19.4; DB 12; Length 132;  
Best Local Similarity 95.2%; Pred. No. 37;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GCAAGTGTCTAGGTGCGGG 21  
|||||||  
FH Key Location/Qualifiers  
  
PT hybridization with probe.  
XX  
PS Claim 6; SEQ ID NO 13; 47bp; Japanese.  
XX  
CC The invention comprises a method for detecting a target nucleic acid. The  
CC method of the invention is useful for: single nucleotide polymorphism  
CC detection, diagnosis of disease by analysing disease-related genes,  
CC estimating risk of incidence of the disease, detection of infection,  
CC analysing virus types, and in toxicity studies. The present DNA sequence  
CC represents a PCR primer of the invention.  
XX  
SQ Sequence 46 BP; 7 A; 9 C; 19 G; 11 T; 0 U; 0 Other;  
  
Query Match 92.4%; Score 19.4; DB 12; Length 46;  
Best Local Similarity 95.2%; Pred. No. 34;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GCAAGTGTCTAGGTGCGGG 21  
DB 4 GCAAGTGTCTAGGTGCGGG 24  
  
RESULT 8  
ADO78057/c  
ID ADO78057 standard; DNA; 132 BP.  
XX  
AC ADO78057;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Human MxA gene promoter region #2.  
XX  
KW nucleic acid analysis; single nucleotide polymorphism detection;  
KW SNP detection; human; MxA; promoter; ds.  
XX  
OS Homo sapiens.  
XX  
PN JP2004121044-A.  
XX  
PD 22-APR-2004.  
XX  
PF 30-SEP-2002; 2002JP-00287376.  
XX  
PR 30-SEP-2002; 2002JP-00287376.  
XX  
PA (TOKE ) TOSHIBA KK.  
XX  
DR WPI; 2004-322749/30.  
XX  
PT Analyzing nucleic acid sequence, involves allowing nucleic acid in sample  
PT to react and hybridize with first and second probe having homologous  
XX sequence except for single base at target region.  
XX  
PS Example 1; SEQ ID NO 2; 16pp; Japanese.  
XX  
CC The invention comprises a method for analysing a nucleic acid sequence,  
CC the method involves allowing the nucleic acid in a sample to hybridise  
CC with a first probe and a second probe which is shorter than the first  
CC probe by one base, where the sequence of the first and second probe are  
CC homologous except for a single base at the target region. The method of  
CC the invention is useful for analysing nucleic acid sequences (e.g. single  
CC nucleotide polymorphism detection). The present DNA sequence represents a  
CC region of the human MxA gene promoter which was used in an example of the  
CC invention.  
XX  
SQ Sequence 132 BP; 22 A; 46 C; 38 G; 26 T; 0 U; 0 Other;  
  
Query Match 92.4%; Score 19.4; DB 12; Length 132;  
Best Local Similarity 95.2%; Pred. No. 37;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GCAAGTGTCTAGGTGCGGG 21  
|||||||  
FH Key Location/Qualifiers

Db 31 GCAAGTGTCTAGGTGCGGG 11  
  
RESULT 9  
ADO78056/c  
ID ADO78056 standard; DNA; 132 BP.  
XX  
AC ADO78056;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Human MxA gene promoter region #1.  
XX  
KW nucleic acid analysis; single nucleotide polymorphism detection;  
KW SNP detection; human; MxA; promoter; ds.  
XX  
OS Homo sapiens.  
XX  
PN JP2004121044-A.  
XX  
PD 22-APR-2004.  
XX  
PF 30-SEP-2002; 2002JP-00287376.  
XX  
PR 30-SEP-2002; 2002JP-00287376.  
XX  
PA (TOKE ) TOSHIBA KK.  
XX  
DR WPI; 2004-322749/30.  
XX  
PT Analyzing nucleic acid sequence, involves allowing nucleic acid in sample  
PT to react and hybridize with first and second probe having homologous  
XX sequence except for single base at target region.  
XX  
PS Example 1; SEQ ID NO 1; 16pp; Japanese.  
XX  
CC The invention comprises a method for analysing a nucleic acid sequence,  
CC the method involves allowing the nucleic acid in a sample to hybridise  
CC with a first probe and a second probe which is shorter than the first  
CC probe by one base, where the sequence of the first and second probe are  
CC homologous except for a single base at the target region. The method of  
CC the invention is useful for analysing nucleic acid sequences (e.g. single  
CC nucleotide polymorphism detection). The present DNA sequence represents a  
CC region of the human MxA gene promoter which was used in an example of the  
CC invention.  
XX  
SQ Sequence 132 BP; 22 A; 46 C; 39 G; 25 T; 0 U; 0 Other;  
  
Query Match 92.4%; Score 19.4; DB 12; Length 132;  
Best Local Similarity 95.2%; Pred. No. 37;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GCAAGTGTCTAGGTGCGGG 21  
|||||||  
DB 31 GCAAGTGTCTAGGTGCGGG 11  
  
RESULT 10  
AAI70373  
ID AAI70373 standard; DNA; 581 BP.  
XX  
AC AAI70373;  
XX  
DT 07-JAN-2002 (first entry)  
XX  
DE Human MxA gene promoter region (thymine variant).  
XX  
KW MxA gene; human; promoter; interferon; therapy; hepatitis C virus;  
KW polymorphism; gene therapy; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers

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FT misc_feature 441..456
FT /*tag= a
FT /function= "interferon-stimulated response element"
FT replace(455,V)
FT variation
FT /*tag= b
FT /standard_name= "single nucleotide polymorphism"
XX PN EP1136571-A2.
XX PD 26-SEP-2001.
XX XX
XX PF 22-MAR-2001; 2001EP-00302708.
XX PR 22-MAR-2000; 2000JP-00080955.
XX PR 06-MAR-2001; 2001JP-00062371.
XX PA (TOKE ) TOSHIBA KK.
XX PI Hijikata M, Mishiro S, Oota Y, Hashimoto K;
XX WPI; 2001-640393/74.
XX DR New polynucleotides, useful for predicting validity of interferon in
XX PT individual infected with hepatitis C virus and in gene therapy for
XX PT interferon therapy, comprises polymorphisms in MxA gene.
XX PS Claim 1; Page 13; 25pp; English.
XX CC The present sequence is that of the promoter region of the human MxA
XX CC gene. The promoter includes an interferon-stimulated response element
XX CC (ISRE). The identity of a single nucleotide polymorphism (SNP) within the
XX CC ISRE affects the sensitivity of an individual to interferon therapy. The
XX CC therapy is valid when the SNP nucleotide is thymine and invalid when the
XX CC SNP nucleotide is guanine, adenine or cytosine. In the present sequence,
XX CC the nucleotide at the SNP site is thymine. Polynucleotides of the
XX CC invention, which comprise the MxA promoter having thymine, guanine,
XX CC adenine or cytosine at the SNP site, or which comprise the corresponding
XX CC ISRE, modified or complementary polynucleotides, can be used to predict
XX CC the validity of interferon therapy for an individual, especially an
XX CC individual infected with hepatitis C virus (claimed). The polynucleotide
XX CC which has thymine at the SNP site can also be used in gene therapy, to
XX CC render an interferon-insensitive individual to be interferon-sensitive
XX CC (also claimed)
XX SQ Sequence 581 BP; 118 A; 147 C; 214 G; 101 T; 0 U; 1 Other;
XX
XX Query Match 92.4%; Score 19.4; DB 4; Length 581;
XX Best Local Similarity 95.2%; Pred. No. 41;
XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 GCAAGTGCTGTAGTGCGGGG 21
DB 410 GCAAGTGCTGTAGTGCGGGG 430
XX
RESULT 11
AAI70375
ID AAI70375 standard; DNA; 581 BP.
XX AC AAI70375;
XX DT 07-JAN-2002 (first entry)
XX DE Human MxA gene promoter region (adenine variant).
XX KW MxA gene; human; promoter; interferon; therapy; hepatitis C virus;
XX KW polymorphism; gene therapy; ds.
XX OS Homo sapiens.
XX PH Key Location/Qualifiers
XX FT misc_feature 441..456
XX FT /*tag= a
XX FT
```

```
FT variation
FT /function= "interferon-stimulated response element"
FT replace(455,B)
FT /*tag= b
FT /standard_name= "single nucleotide polymorphism"
XX PN EP1136571-A2.
XX PD 26-SEP-2001.
XX XX
XX PF 22-MAR-2001; 2001EP-00302708.
XX PR 22-MAR-2000; 2000JP-00080955.
XX PR 06-MAR-2001; 2001JP-00062371.
XX PA (TOKE ) TOSHIBA KK.
XX PI Hijikata M, Mishiro S, Oota Y, Hashimoto K;
XX WPI; 2001-640393/74.
XX DR New polynucleotides, useful for predicting validity of interferon in
XX PT individual infected with hepatitis C virus and in gene therapy for
XX PT interferon therapy, comprises polymorphisms in MxA gene.
XX PS Claim 3; Page 14; 25pp; English.
XX CC The present sequence is that of the promoter region of the human MxA
XX CC gene. The promoter includes an interferon-stimulated response element
XX CC (ISRE). The identity of a single nucleotide polymorphism (SNP) within the
XX CC ISRE affects the sensitivity of an individual to interferon therapy. The
XX CC therapy is valid when the SNP nucleotide is thymine and invalid when the
XX CC SNP nucleotide is guanine, adenine or cytosine. In the present sequence,
XX CC the nucleotide at the SNP site is adenine. Polynucleotides of the
XX CC invention, which comprise the MxA promoter having thymine, guanine,
XX CC adenine or cytosine at the SNP site, or which comprise the corresponding
XX CC ISRE, modified or complementary polynucleotides, can be used to predict
XX CC the validity of interferon therapy for an individual, especially an
XX CC individual infected with hepatitis C virus (claimed). The polynucleotide
XX CC which has thymine at the SNP site (see AAI70373) can also be used in gene
XX CC therapy, to render an interferon-insensitive individual to be interferon-
XX CC sensitive (also claimed)
XX SQ Sequence 581 BP; 119 A; 147 C; 214 G; 100 T; 0 U; 1 Other;
XX
XX Query Match 92.4%; Score 19.4; DB 4; Length 581;
XX Best Local Similarity 95.2%; Pred. No. 41;
XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 GCAAGTGCTGTAGTGCGGGG 21
DB 410 GCAAGTGCTGTAGTGCGGGG 430
XX
RESULT 12
AAI70376
ID AAI70376 standard; DNA; 581 BP.
XX AC AAI70376;
XX DT 07-JAN-2002 (first entry)
XX DE Human MxA gene promoter region (cytosine variant).
XX KW MxA gene; human; promoter; interferon; therapy; hepatitis C virus;
XX KW polymorphism; gene therapy; ds.
XX OS Homo sapiens.
XX PH Key Location/Qualifiers
XX FT misc_feature 441..456
XX FT /*tag= a
XX FT /function= "interferon-stimulated response element"
XX FT replace(455,D)
XX FT
```

```
FT FT /*tag= b
XX XX /standard_name= "single nucleotide polymorphism"
PN PN
XX EP1136571-A2.
PD PD
XX 26-SEP-2001.
XX
XX 22-MAR-2001; 2001EP-00302708.
XX
XX 22-MAR-2000; 2000JP-00080955.
XX
XX 06-MAR-2001; 2001JP-00062371.
XX
XX (TOKE ) TOSHIBA KK.
XX
XX Hijikata M, Mishihiro S, Oota Y, Hashimoto K;
XX
XX WPI; 2001-640393/74.
XX
XX New polynucleotides, useful for predicting validity of interferon in
XX individual infected with hepatitis C virus and in gene therapy for
XX interferon therapy, comprises polymorphisms in MxA gene.
XX
XX Claim 3; Page 14; 25pp; English.
XX
XX The present sequence is that of the promoter region of the human MxA
XX gene. The promoter includes an interferon-stimulated response element
XX (ISRE). The identity of a single nucleotide polymorphism (SNP) within the
XX ISRE affects the sensitivity of an individual to interferon therapy. The
XX therapy is valid when the SNP nucleotide is thymine and invalid when the
XX SNP nucleotide is guanine, adenine or cytosine. In the present sequence,
XX the nucleotide at the SNP site is cytosine. Polynucleotides of the
XX invention, which comprise the MxA promoter having thymine, guanine,
XX adenine or cytosine at the SNP site, or which comprise the corresponding
XX ISRE, modified or complementary polynucleotides, can be used to predict
XX the validity of interferon therapy for an individual, especially an
XX individual infected with hepatitis C virus (claimed). The polynucleotide
XX which has thymine at the SNP site (see AAI70373) can also be used in gene
XX therapy, to render an interferon-insensitive individual to be interferon-
XX sensitive (also claimed)
XX
XX Sequence 581 BP; 118 A; 148 C; 214 G; 100 T; 0 U; 1 Other;
XX
XX Query Match 92.4%; Score 19.4; DB 4; Length 581;
XX Best Local Similarity 95.2%; Pred. No. 41;
XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 GCAAGTGTCTGAGGTGCGGG 21
XX ||||||| |||||||
XX Db 410 GCAAGTGTCTGAGGTGCGGG 430
XX
XX RESULT 13
XX AAI70374
XX ID AAI70374 standard; DNA; 581 BP.
XX
XX AC AAI70374;
XX
XX DT 07-JAN-2002 (first entry)
XX
XX DE Human MxA gene promoter region (guanine variant).
XX
XX MxA gene; human; promoter; interferon; therapy; hepatitis C virus;
XX polymorphism; gene therapy; ds.
XX
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH misc_feature 441..456
XX FT /*tag= a
XX FT /function= "interferon-stimulated response element"
XX FT replace(455,H)
XX FT /*tag= b
XX FT /standard_name= "single nucleotide polymorphism"
XX FT
```

```
XX
XX EP1136571-A2.
XX
XX 26-SEP-2001.
XX
XX 22-MAR-2001; 2001EP-00302708.
XX
XX 22-MAR-2000; 2000JP-00080955.
XX
XX 06-MAR-2001; 2001JP-00062371.
XX
XX (TOKE ) TOSHIBA KK.
XX
XX Hijikata M, Mishihiro S, Oota Y, Hashimoto K;
XX
XX WPI; 2001-640393/74.
XX
XX New polynucleotides, useful for predicting validity of interferon in
XX individual infected with hepatitis C virus and in gene therapy for
XX interferon therapy, comprises polymorphisms in MxA gene.
XX
XX Claim 2; Page 14; 25pp; English.
XX
XX The present sequence is that of the promoter region of the human MxA
XX gene. The promoter includes an interferon-stimulated response element
XX (ISRE). The identity of a single nucleotide polymorphism (SNP) within the
XX ISRE affects the sensitivity of an individual to interferon therapy. The
XX therapy is valid when the SNP nucleotide is thymine and invalid when the
XX SNP nucleotide is guanine, adenine or cytosine. In the present sequence,
XX the nucleotide at the SNP site is guanine. Polynucleotides of the
XX invention, which comprise the MxA promoter having thymine, guanine,
XX adenine or cytosine at the SNP site, or which comprise the corresponding
XX ISRE, modified or complementary polynucleotides, can be used to predict
XX the validity of interferon therapy for an individual, especially an
XX individual infected with hepatitis C virus (claimed). The polynucleotide
XX which has thymine at the SNP site (see AAI70373) can also be used in gene
XX therapy, to render an interferon-insensitive individual to be interferon-
XX sensitive (also claimed)
XX
XX Sequence 581 BP; 118 A; 147 C; 215 G; 100 T; 0 U; 1 Other;
XX
XX Query Match 92.4%; Score 19.4; DB 4; Length 581;
XX Best Local Similarity 95.2%; Pred. No. 41;
XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 GCAAGTGTCTGAGGTGCGGG 21
XX ||||||| |||||||
XX Db 410 GCAAGTGTCTGAGGTGCGGG 430
XX
XX RESULT 14
XX AAI70353
XX ID AAI70353 standard; DNA; 581 BP.
XX
XX AC AAI70353;
XX
XX DT 07-JAN-2002 (first entry)
XX
XX DE Promoter region of human MxA gene (C at position 455).
XX
XX MxA gene; human; promoter; interferon; therapy; validation;
XX gene detection; hepatitis C virus; DNA chip; ds.
XX
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH misc_feature 441..456
XX FT /*tag= a
XX FT /function= "interferon-stimulated response element"
XX FT replace(455,D)
XX FT /*tag= b
XX FT /standard_name= "single nucleotide polymorphism"
XX FT
XX EP1136570-A2.
```

```

XX PD 26-SEP-2001.
XX PF
XX PF 22-MAR-2001; 2001EP-00302705.
XX PR 22-MAR-2000; 2000JP-00080955.
XX PR 06-MAR-2001; 2001JP-00062372.
XX PA (TOKE ) TOSHIBA KK.
XX PI Hijitaka M, Mishiro S, Oota Y, Hashimoto K;
XX WPI; 2001-640392/74.
XX DR
XX PT New carriers for gene detection, particularly useful for detecting
XX PT validity of interferon therapy, especially in a patient infected with
XX PT hepatitis C virus.
XX PS Claim 4; Page 19; 33pp; English.
XX CC The present sequence is that of the promoter region of the human MxA
XX CC gene, in which the 15th position of an interferon-stimulated response
XX CC element (ISRE) is cytosine. A single nucleotide polymorphism (SNP) at
XX CC this site affects the sensitivity of an individual to interferon therapy.
XX CC Interferon therapy is less effective for individuals having an ISRE which
XX CC is not either T/T homozygous or T/non-T heterozygous at this site. Use of
XX CC carriers for gene detection of the present invention allows examination
XX CC of whether the SNP site in the MxA gene promoter from a subject is
XX CC thymine or not. The method uses a carrier for gene detection comprising a
XX CC base body onto which a polynucleotide is immobilized. The polynucleotide
XX CC may comprise the present sequence, a modified polynucleotide derived from
XX CC it, a polynucleotide spanning positions 441-455 or positions 449-459, or
XX CC a polynucleotide complementary to any of these. A DNA chip for use in
XX CC gene detection is also claimed. Detection of hybridisation with a
XX CC polynucleotide taken e.g. from a hepatitis C virus-infected individual
XX CC may be carried out by detecting an electrochemical change that
XX CC accompanies hybridisation
XX CC
XX CC Sequence 581 BP; 118 A; 148 C; 214 G; 100 T; 0 U; 1 Other;
XX SQ
XX
Query Match 92.4%; Score 19.4; DB 5; Length 581;
Best Local Similarity 95.2%; Pred. No. 41;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGCTAGGTGCGGG 21
Db 410 GCAAGTGCTGCTAGGTGCGGG 430

RESULT 15
AAI70350
ID AAI70350 standard; DNA; 581 BP.
XX AC
XX AAI70350;
XX DT
XX 07-JAN-2002 (first entry)
XX DE
XX Promoter region of human MxA gene (T at position 455).
XX MxA gene; human; promoter; interferon; therapy; validation;
XX gene detection; hepatitis C virus; DNA chip; ds.
XX Homo sapiens.
XX Key Location/Qualifiers
XX misc_feature 441..456
XX /tag= a
XX /function= "interferon-stimulated response element"
XX variation
XX /replace(455,v)
XX /tag= b
XX /standard_name= "single nucleotide polymorphism"
XX PN EPI136570-A2.

```

```

XX PD 26-SEP-2001.
XX PF
XX PF 22-MAR-2001; 2001EP-00302705.
XX PR 22-MAR-2000; 2000JP-00080955.
XX PR 06-MAR-2001; 2001JP-00062372.
XX PA (TOKE ) TOSHIBA KK.
XX PI Hijitaka M, Mishiro S, Oota Y, Hashimoto K;
XX WPI; 2001-640392/74.
XX DR
XX PT New carriers for gene detection, particularly useful for detecting
XX PT validity of interferon therapy, especially in a patient infected with
XX PT hepatitis C virus.
XX PS Claim 1; Page 18; 33pp; English.
XX CC The present sequence is that of the promoter region of the human MxA
XX CC gene, in which the 15th position of an interferon-stimulated response
XX CC element (ISRE) is thymine. A single nucleotide polymorphism (SNP) at this
XX CC site affects the sensitivity of an individual to interferon therapy.
XX CC Interferon therapy is more effective for individuals having an ISRE which
XX CC is either T/T homozygous or T/non-T heterozygous at this site. Use of
XX CC carriers for gene detection of the present invention allows examination
XX CC of whether the SNP site in the MxA gene promoter from a subject is
XX CC thymine or not. The method uses a carrier for gene detection comprising a
XX CC base body onto which a polynucleotide is immobilized. The polynucleotide
XX CC may comprise the present sequence, a modified polynucleotide derived from
XX CC it, a polynucleotide spanning positions 441-455 or positions 449-459, or
XX CC a polynucleotide complementary to any of these. A DNA chip is also
XX CC claimed. Detection of hybridisation with a polynucleotide taken e.g. from
XX CC a hepatitis C virus-infected individual may be carried out by detecting
XX CC an electrochemical change that accompanies the hybridisation
XX CC
XX CC Sequence 581 BP; 118 A; 147 C; 214 G; 101 T; 0 U; 1 Other;
XX SQ
XX
Query Match 92.4%; Score 19.4; DB 5; Length 581;
Best Local Similarity 95.2%; Pred. No. 41;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGCTAGGTGCGGG 21
Db 410 GCAAGTGCTGCTAGGTGCGGG 430

RESULT 16
AAI70352
ID AAI70352 standard; DNA; 581 BP.
XX AC
XX AAI70352;
XX DT
XX 07-JAN-2002 (first entry)
XX DE
XX Promoter region of human MxA gene (A at position 455).
XX MxA gene; human; promoter; interferon; therapy; validation;
XX gene detection; hepatitis C virus; DNA chip; ds.
XX Homo sapiens.
XX Key Location/Qualifiers
XX misc_feature 441..456
XX /tag= a
XX /function= "interferon-stimulated response element"
XX variation
XX /replace(455,B)
XX /tag= b
XX /standard_name= "single nucleotide polymorphism"
XX PN EPI136570-A2.

```



XX DR WPI; 2003-040593/03.

XX PT Detecting nucleic acids relating diseases particularly due to pathogenic

XX PT microorganisms e.g. hepatitis, influenza and AIDS in individuals from

PT PT their data using immobilized probes on substrate, also for therapeutic

PT PT evaluation.

XX PS Claim 15; Page 95; 125pp; Japanese.

XX CC This invention relates to a method for obtaining first data on a nucleic

CC CC acid from an individual exposed to a specific disease and second data on

CC CC a nucleic acid from a pathogenic microorganism occurring in the

CC CC individual in order to relate the specific disease to such pathogenic

CC CC microorganism. The method of the invention comprises the reaction of a

CC CC nucleic acid extract from the individual with a probe-immobilization

CC CC substrate containing first and second probes for detection of the

CC CC pathogenic microorganism with the first probe to relate to the specific

CC CC microbe-caused disease, and the second probe for detecting a specific

CC CC nucleic acid in the individual and obtaining first data from the reaction

CC CC results as well as the detected binding of a nucleic acid with the first

CC CC probe and/or second data from the detected binding of a nucleic acid with

CC CC the second probe. The method of the invention is useful for detecting

CC CC nucleic acids relating diseases particularly due to pathogenic

CC CC microorganisms e.g. hepatitis C, influenza and AIDS in individuals, and

CC CC also for therapeutic evaluation. Such a method is convenient and accurate

CC CC and may be used to design specific therapy for effective treatment even

CC CC for individual patients in a tailor-made manner. The present sequence

CC CC represents a nucleic acid sequence used in the scope of the invention

XX SQ Sequence 581 BP; 118 A; 148 C; 214 G; 100 T; 0 U; 1 Other;

Query Match 92.4%; Score 19.4; DB 10; Length 581;

Best Local Similarity 95.2%; Pred. No. 41;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGGCGGG 21

DB 410 GCAAGTGTCTAGTGGCGGG 430

RESULT 19

ABX08704

ID ABX08704 standard; DNA; 581 BP.

AC ABX08704;

XX 20-JAN-2003 (first entry)

XX Pathogenic organism detection method associated DNA sequence #6.

XX Gene; ss; hepatitis C virus; human; pathogenic microorganism; influenza;

XX AIDS; acquired immunodeficiency syndrome.

XX Homo sapiens.

XX WO200277281-A1.

XX 03-OCT-2002.

XX 05-MAR-2002; 2002WO-JP002030.

XX 27-MAR-2001; 2001JP-00090053.

XX 18-SEP-2001; 2001JP-00284112.

XX (TOKE ) TOSHIBA KK.

XX Hashimoto K, Hashimoto M, Mishiro S, Oota Y;

XX WPI; 2003-040593/03.

XX Detecting nucleic acids relating diseases particularly due to pathogenic

PT PT microorganisms e.g. hepatitis, influenza and AIDS in individuals from

PT their data using immobilized probes on substrate, also for therapeutic

PT evaluation.

XX Claim 15; Page 94; 125pp; Japanese.

XX CC This invention relates to a method for obtaining first data on a nucleic

CC CC acid from an individual exposed to a specific disease and second data on

CC CC a nucleic acid from a pathogenic microorganism occurring in the

CC CC individual in order to relate the specific disease to such pathogenic

CC CC microorganism. The method of the invention comprises the reaction of a

CC CC nucleic acid extract from the individual with a probe-immobilization

CC CC substrate containing first and second probes for detection of the

CC CC pathogenic microorganism with the first probe to relate to the specific

CC CC microbe-caused disease, and the second probe for detecting a specific

CC CC nucleic acid in the individual and obtaining first data from the reaction

CC CC results as well as the detected binding of a nucleic acid with the first

CC CC probe and/or second data from the detected binding of a nucleic acid with

CC CC the second probe. The method of the invention is useful for detecting

CC CC nucleic acids relating diseases particularly due to pathogenic

CC CC microorganisms e.g. hepatitis C, influenza and AIDS in individuals, and

CC CC also for therapeutic evaluation. Such a method is convenient and accurate

CC CC and may be used to design specific therapy for effective treatment even

CC CC for individual patients in a tailor-made manner. The present sequence

CC CC represents a nucleic acid sequence used in the scope of the invention

XX SQ Sequence 581 BP; 118 A; 147 C; 215 G; 100 T; 0 U; 1 Other;

Query Match 92.4%; Score 19.4; DB 10; Length 581;

Best Local Similarity 95.2%; Pred. No. 41;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGGCGGG 21

DB 410 GCAAGTGTCTAGTGGCGGG 430

RESULT 20

ABX08705

ID ABX08705 standard; DNA; 581 BP.

XX AC ABX08705;

XX 20-JAN-2003 (first entry)

XX Pathogenic organism detection method associated DNA sequence #7.

XX Gene; ss; hepatitis C virus; human; pathogenic microorganism; influenza;

XX AIDS; acquired immunodeficiency syndrome.

XX Homo sapiens.

XX WO200277281-A1.

XX 03-OCT-2002.

XX 05-MAR-2002; 2002WO-JP002030.

XX 27-MAR-2001; 2001JP-00090053.

XX 18-SEP-2001; 2001JP-00284112.

XX (TOKE ) TOSHIBA KK.

XX Hashimoto K, Hashimoto M, Mishiro S, Oota Y;

XX WPI; 2003-040593/03.

XX Detecting nucleic acids relating diseases particularly due to pathogenic

PT PT microorganisms e.g. hepatitis, influenza and AIDS in individuals from

PT PT their data using immobilized probes on substrate, also for therapeutic

PT PT evaluation.

XX Claim 15; Page 94-95; 125pp; Japanese.



CC This invention relates to a method for obtaining first data on a nucleic  
CC acid from an individual exposed to a specific disease and second data on  
CC a nucleic acid from a pathogenic microorganism occurring in the  
CC individual in order to relate the specific disease to such pathogenic  
CC microorganism. The method of the invention comprises the reaction of a  
CC nucleic acid extract from the individual with a probe-immobilization  
CC substrate containing first and second probes for detection of the  
CC pathogenic microorganism with the first probe to relate to the specific  
CC microbe-caused disease, and the second probe for detecting a specific  
CC nucleic acid in the individual and obtaining first data from the reaction  
CC results as well as the detected binding of a nucleic acid with the first  
CC probe and/or second data from the detected binding of a nucleic acid with  
CC the second probe. The method of the invention is useful for detecting  
CC nucleic acids relating diseases particularly due to pathogenic  
CC microorganisms e.g. hepatitis C, influenza and AIDS in individuals, and  
CC also for therapeutic evaluation. Such a method is convenient and accurate  
CC and may be used to design specific therapy for effective treatment even  
CC for individual patients in a tailor-made manner. The present sequence  
CC represents a nucleic acid sequence used in the scope of the invention  
XX

XX SQ Sequence 581 BP; 119 A; 147 C; 214 G; 100 T; 0 U; 1 Other;

Query Match 92.4%; Score 19.4; DB 10; Length 581;  
Best Local Similarity 95.2%; Pred. No. 41;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 21  
|||||  
DB 410 GCAAGTGTCTAGGTGCGGG 430

## RESULT 21

ADL92270  
ID ADL92270 standard; DNA; 581 BP.

XX AC ADL92270;

XX DT 20-MAY-2004 (first entry)

XX DE Human MxA gene DNA sequence #8.

XX KW nucleic acid detection; immobilised nucleic acid probe;  
KW single nucleotide polymorphism detection; SNP detection;  
XX disease diagnosis; ds; human; MxA gene.

XX OS Homo sapiens.

XX PN JP2004041109-A.

XX PD 12-FEB-2004.

XX PF 12-JUL-2002; 2002JP-00204444.

XX PR 12-JUL-2002; 2002JP-00204444.

XX PA (TOKE ) TOSHIBA KK.

XX DR WPI; 2004-151026/15.

XX PT Detecting target nucleic acid (T) using probe, comprises amplifying  
PT target sequence (S) so that end of (S) which is hybridized with probe is  
PT positioned at less than 40 bases from terminal base of (T) and detecting  
XX hybridization with probe.

XX PS Disclosure; SEQ ID NO 27; 47pp; Japanese.

XX CC The invention comprises a method for detecting a target nucleic acid. The  
CC method of the invention is useful for: single nucleotide polymorphism  
CC detection, diagnosis of disease by analysing disease-related genes,  
CC estimating risk of incidence of the disease, detection of infection,  
CC analysing virus types, and in toxicity studies. The present nucleic acid  
CC represents a human MxA gene DNA sequence which was used in the  
CC exemplification of the invention.

XX

XX SQ Sequence 581 BP; 118 A; 148 C; 214 G; 100 T; 0 U; 1 Other;

Query Match 92.4%; Score 19.4; DB 12; Length 581;  
Best Local Similarity 95.2%; Pred. No. 41;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 21  
|||||  
DB 410 GCAAGTGTCTAGGTGCGGG 430

## RESULT 22

ADL92267

ID ADL92267 standard; DNA; 581 BP.

XX AC ADL92267;

XX DT 20-MAY-2004 (first entry)

XX DE Human MxA gene DNA sequence #5.

XX KW nucleic acid detection; immobilised nucleic acid probe;  
KW single nucleotide polymorphism detection; SNP detection;  
XX disease diagnosis; ds; human; MxA gene.

XX OS Homo sapiens.

XX PN JP2004041109-A.

XX PD 12-FEB-2004.

XX PF 12-JUL-2002; 2002JP-00204444.

XX PR 12-JUL-2002; 2002JP-00204444.

XX PA (TOKE ) TOSHIBA KK.

XX DR WPI; 2004-151026/15.

XX PT Detecting target nucleic acid (T) using probe, comprises amplifying  
PT target sequence (S) so that end of (S) which is hybridized with probe is  
PT positioned at less than 40 bases from terminal base of (T) and detecting  
XX hybridization with probe.

XX PS Disclosure; SEQ ID NO 24; 47pp; Japanese.

XX CC The invention comprises a method for detecting a target nucleic acid. The  
CC method of the invention is useful for: single nucleotide polymorphism  
CC detection, diagnosis of disease by analysing disease-related genes,  
CC estimating risk of incidence of the disease, detection of infection,  
CC analysing virus types, and in toxicity studies. The present nucleic acid  
CC represents a human MxA gene DNA sequence which was used in the  
CC exemplification of the invention.

XX SQ Sequence 581 BP; 119 A; 147 C; 213 G; 101 T; 0 U; 1 Other;

Query Match 92.4%; Score 19.4; DB 12; Length 581;  
Best Local Similarity 95.2%; Pred. No. 41;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGGTGCGGG 21  
|||||  
DB 410 GCAAGTGTCTAGGTGCGGG 430

## RESULT 23

AAD55993

ID AAD55993 standard; DNA; 2451 BP.

XX AC AAD55993;

XX DT 07-AUG-2003 (first entry)

XX Human MxA domain DNA.  
DE MxA; GTPase; cancer; gene therapy; cytostatic; human; gene; ds.  
XX Homo sapiens.  
XX WO2003033667-A2.  
XX 24-APR-2003.  
XX 18-OCT-2002; 2002WO-US033232.  
XX 18-OCT-2001; 2001US-0329740P.  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX Mushinski FJ, Trepel JB, Horisberger MA, Nguyen P, Khanna C;  
XX WPI; 2003-393519/37.  
XX  
XX Use of a polypeptide having at least 90% amino acid sequence identity to  
PT human MxA or a nucleic acid encoding the protein in preparing a  
PT medicament for reducing cancer progression in a mammal.  
XX Disclosure; Page 57-58; 62pp; English.  
XX The invention relates to the use of a polypeptide having at least 90%  
CC amino acid sequence identity to human MxA or a nucleic acid encoding the  
CC protein. Mx proteins belong to a family of unique GTPases. The invention  
CC is used for preparing a medicament for reducing cancer progression in a  
CC mammal. It is also used in gene therapy. The present sequence is human  
CC MxA domain encoding DNA used in the invention  
XX  
XX Sequence 2451 BP; 591 A; 553 C; 704 G; 603 T; 0 U; 0 Other;  
SQ  
Query Match 92.4%; Score 19.4; DB 9; Length 2451;  
Best Local Similarity 95.2%; Pred. No. 46;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GCAAGTCTGTAGTGGGGG 21  
DB 2398 GCAAGTCTGTAGTGGGGG 2418  
RESULT 24  
AAD55995  
ID AAD55995 standard; DNA; 5376 BP.  
AC AAD55995;  
XX 07-AUG-2003 (first entry)  
XX Luciferase gene.  
XX MxA; GTPase; cancer; gene therapy; cytostatic; luciferase; enzyme; gene;  
XX ds.  
XX Unidentified.  
XX WO2003033667-A2.  
XX 24-APR-2003.  
XX 18-OCT-2002; 2002WO-US033232.  
XX 18-OCT-2001; 2001US-0329740P.  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX Mushinski FJ, Trepel JB, Horisberger MA, Nguyen P, Khanna C;  
XX WPI; 2003-393519/37.  
XX

XX Use of a polypeptide having at least 90% amino acid sequence identity to  
PT human MxA or a nucleic acid encoding the protein in preparing a  
PT medicament for reducing cancer progression in a mammal.  
XX Example 7; Page 59-61; 62pp; English.  
XX The invention relates to the use of a polypeptide having at least 90%  
CC amino acid sequence identity to human MxA or a nucleic acid encoding the  
CC protein. Mx proteins belong to a family of unique GTPases. The invention  
CC is used for preparing a medicament for reducing cancer progression in a  
CC mammal. It is also used in gene therapy. The present sequence is  
CC luciferase gene used in the invention  
XX  
XX Sequence 5376 BP; 1365 A; 1282 C; 1368 G; 1361 T; 0 U; 0 Other;  
SQ  
Query Match 92.4%; Score 19.4; DB 9; Length 5376;  
Best Local Similarity 95.2%; Pred. No. 48;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GCAAGTCTGTAGTGGGGG 21  
DB 444 GCAAGTCTGTAGTGGGGG 464  
RESULT 25  
AEB96544  
ID AEB96544 standard; DNA; 49343 BP.  
XX AEB96544;  
XX 06-OCT-2005 (first entry)  
XX Human MX1 gene, SEQ ID 28.  
XX hepatitis C virus infection; antiinflammatory; hepatotropic; virucide;  
XX liver cirrhosis; fibrosis; hepatoma; SNP detection; MX1; ds.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FH variation 1563  
FT /\*tag= a "Single nucleotide polymorphism"  
FT /standard\_name= 2802  
FT variation /\*tag= b "Single nucleotide polymorphism"  
FT /standard\_name= 2869  
FT variation /\*tag= c "Single nucleotide polymorphism"  
FT /standard\_name= 3159  
FT variation /\*tag= d "Single nucleotide polymorphism"  
FT /standard\_name= 3836  
FT variation /\*tag= e "Single nucleotide polymorphism"  
FT /standard\_name= 4105  
FT variation /\*tag= f "Single nucleotide polymorphism"  
FT /standard\_name= 5232  
FT variation /\*tag= g "Single nucleotide polymorphism"  
FT /standard\_name= 5261  
FT variation /\*tag= h "Single nucleotide polymorphism"  
FT /standard\_name= 5558  
FT variation /\*tag= i "Single nucleotide polymorphism"  
FT /standard\_name= 6034  
FT variation /\*tag= j "Single nucleotide polymorphism"  
FT /standard\_name= 6135  
FT variation /\*tag= k

FT	variation	/standard_name= "Single nucleotide polymorphism"	FT	variation	15487
FT		6684	FT		/tag= aj
FT		/tag= l	FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	/standard_name= "Single nucleotide polymorphism"	FT	variation	16581
FT		7143	FT		/tag= ak
FT		/tag= m	FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	/standard_name= "Single nucleotide polymorphism"	FT	variation	16818
FT		7251	FT		/tag= al
FT		/tag= n	FT		/standard_name= "Single nucleotide polymorphism"
FT		/standard_name= "Single nucleotide polymorphism"	FT	variation	17093
FT	variation	/tag= o	FT		/tag= am
FT		7856	FT		/standard_name= "Single nucleotide polymorphism"
FT		/tag= p	FT	variation	17132
FT	variation	/standard_name= "Single nucleotide polymorphism"	FT		/tag= an
FT		9268	FT		/standard_name= "Single nucleotide polymorphism"
FT		/tag= q	FT	variation	17151
FT		/standard_name= "Single nucleotide polymorphism"	FT		/tag= ao
FT	variation	/tag= r	FT		/standard_name= "Single nucleotide polymorphism"
FT		9392	FT	variation	17190
FT		/tag= s	FT		/tag= ap
FT		/standard_name= "Single nucleotide polymorphism"	FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	/tag= t	FT	variation	17278
FT		10001	FT		/tag= aq
FT		/tag= u	FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	/tag= v	FT		/tag= ar
FT		10206	FT		/standard_name= "Single nucleotide polymorphism"
FT		/tag= w	FT	variation	18284
FT	variation	/tag= x	FT		/tag= at
FT		12604	FT		/standard_name= "Single nucleotide polymorphism"
FT		/tag= y	FT	variation	18479
FT	variation	/standard_name= "Single nucleotide polymorphism"	FT		/tag= au
FT		12693	FT		/standard_name= "Single nucleotide polymorphism"
FT		/tag= z	FT	variation	18624
FT	variation	/standard_name= "Single nucleotide polymorphism"	FT		/tag= av
FT		12918	FT		/standard_name= "Single nucleotide polymorphism"
FT		/tag= aa	FT	variation	18799
FT	variation	/tag= ab	FT		/tag= aw
FT		12936	FT		/standard_name= "Single nucleotide polymorphism"
FT		/tag= ac	FT	variation	18882
FT	variation	/standard_name= "Single nucleotide polymorphism"	FT		/tag= ax
FT		13584	FT		/standard_name= "Single nucleotide polymorphism"
FT		/tag= ad	FT	variation	18883
FT	variation	/standard_name= "Single nucleotide polymorphism"	FT		/tag= ay
FT		13757	FT		/standard_name= "Single nucleotide polymorphism"
FT		/tag= ae	FT	variation	19506
FT	variation	/standard_name= "Single nucleotide polymorphism"	FT		/tag= az
FT		14111	FT		/standard_name= "Single nucleotide polymorphism"
FT		/tag= af	FT	variation	19582
FT	variation	/standard_name= "Single nucleotide polymorphism"	FT		/tag= ba
FT		14200	FT		/standard_name= "Single nucleotide polymorphism"
FT		/tag= ag	FT	variation	20110
FT	variation	/standard_name= "Single nucleotide polymorphism"	FT		/tag= bb
FT		15242	FT		/standard_name= "Single nucleotide polymorphism"
FT		/tag= ah	FT	variation	20472
FT	variation	/standard_name= "Single nucleotide polymorphism"	FT		/tag= bc
FT		15245	FT		/standard_name= "Single nucleotide polymorphism"
FT		/tag= ai	FT	variation	20947
FT	variation	/standard_name= "Single nucleotide polymorphism"	FT		/tag= bd
FT			FT		/standard_name= "Single nucleotide polymorphism"
FT			FT	variation	21968
FT			FT		/tag= be
FT			FT		/standard_name= "Single nucleotide polymorphism"
FT			FT	variation	22058
FT			FT		/tag= bf
FT			FT		/standard_name= "Single nucleotide polymorphism"
FT			FT	variation	22136
FT			FT		/tag= bg
FT			FT		/standard_name= "Single nucleotide polymorphism"
FT			FT	variation	23330

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FT      /*tag= bh
FT      /standard_name= "Single nucleotide polymorphism"
FT      variation
FT      2384
FT      /*tag= bi
FT      /standard_name= "Single nucleotide polymorphism"
FT      2388
FT      /*tag= bj
FT      /standard_name= "Single nucleotide polymorphism"

Query Match      92.4%; Score 19.4; DB 14; Length 49343;
Best Local Similarity 95.2%; Pred. No. 57;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCAAGTGTCTAGTGTGGGG 21
Db      7098 GCAAGTGTCTGACAGTGTGGGG 7118

RESULT 26
ADL92263
ID      ADL92263 standard; DNA; 581 BP.
XX
AC      ADL92263;
XX
DT      20-MAY-2004 (first entry)
XX
DE      Human MxA gene DNA sequence #1.
XX
KW      nucleic acid detection; immobilised nucleic acid probe;
KW      single nucleotide polymorphism detection; SNP detection;
KW      disease diagnosis; ds; human; MxA gene.
XX
OS      Homo sapiens.
XX
PN      JP2004041109-A.
XX
PD      12-FEB-2004.
XX
PF      12-JUL-2002; 2002JP-00204444.
XX
PR      12-JUL-2002; 2002JP-00204444.
XX
PS      (TOKE ) TOSHIBA KK.
XX
SQ      Sequence 581 BP; 118 A; 147 C; 213 G; 102 T; 0 U; 1 Other;

Query Match      87.6%; Score 18.4; DB 12; Length 581;
Best Local Similarity 90.5%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

PT      Detecting target nucleic acid (T) using probe, comprises amplifying
PT      target sequence (S) so that end of (S) which is hybridized with probe is
PT      positioned at less than 40 bases from terminal base of (T) and detecting
PT      hybridization with probe.
XX
PS      Disclosure; SEQ ID NO 20; 47pp; Japanese.
XX
SQ      Sequence 581 BP; 118 A; 147 C; 213 G; 102 T; 0 U; 1 Other;

The invention comprises a method for detecting a target nucleic acid. The
method of the invention is useful for: single nucleotide polymorphism
detection, diagnosis of disease by analysing disease-related genes,
estimating risk of incidence of the disease, detection of infection,
analysing virus types, and in toxicity studies. The present nucleic acid
represents a human MxA gene DNA sequence which was used in the
exemplification of the invention.

Query Match      87.6%; Score 18.4; DB 12; Length 581;
Best Local Similarity 90.5%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GCAAGTGTCTAGTGTGGGG 21
Db      410 GCAAGTGTCTGACAGTGTGGGG 7118

RESULT 27
ADL92265
ID      ADL92265 standard; DNA; 581 BP.
XX
AC      ADL92265;
XX
DT      20-MAY-2004 (first entry)
XX
DE      Human MxA gene DNA sequence #3.
XX
KW      nucleic acid detection; immobilised nucleic acid probe;
KW      single nucleotide polymorphism detection; SNP detection;
KW      disease diagnosis; ds; human; MxA gene.
XX
OS      Homo sapiens.
XX
PN      JP2004041109-A.
XX
PD      12-FEB-2004.
XX
```

```
ADL92266
ID      ADL92266 standard; DNA; 581 BP.
XX
AC      ADL92266;
XX
DT      20-MAY-2004 (first entry)
XX
DE      Human MxA gene DNA sequence #4.
XX
KW      nucleic acid detection; immobilised nucleic acid probe;
KW      single nucleotide polymorphism detection; SNP detection;
KW      disease diagnosis; ds; human; MxA gene.
XX
OS      Homo sapiens.
XX
PN      JP2004041109-A.
XX
PD      12-FEB-2004.
XX
PF      12-JUL-2002; 2002JP-00204444.
XX
PR      12-JUL-2002; 2002JP-00204444.
XX
PS      (TOKE ) TOSHIBA KK.
XX
SQ      WPI; 2004-151026/15.

Detecting target nucleic acid (T) using probe, comprises amplifying
target sequence (S) so that end of (S) which is hybridized with probe is
positioned at less than 40 bases from terminal base of (T) and detecting
hybridization with probe.
XX
PS      Disclosure; SEQ ID NO 23; 47pp; Japanese.
XX
SQ      Sequence 581 BP; 118 A; 149 C; 213 G; 100 T; 0 U; 1 Other;

Query Match      87.6%; Score 18.4; DB 12; Length 581;
Best Local Similarity 90.5%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GCAAGTGTCTAGTGTGGGG 21
Db      410 GCAAGTGTCTGACAGTGTGGGG 430

RESULT 28
ADL92265
ID      ADL92265 standard; DNA; 581 BP.
XX
AC      ADL92265;
XX
DT      20-MAY-2004 (first entry)
XX
DE      Human MxA gene DNA sequence #3.
XX
KW      nucleic acid detection; immobilised nucleic acid probe;
KW      single nucleotide polymorphism detection; SNP detection;
KW      disease diagnosis; ds; human; MxA gene.
XX
OS      Homo sapiens.
XX
PN      JP2004041109-A.
XX
PD      12-FEB-2004.
XX
```

PF 12-JUL-2002; 2002JP-00204444.  
XX  
PR 12-JUL-2002; 2002JP-00204444.  
XX  
PA (TOKE ) TOSHIBA KK.  
XX  
XX WPI; 2004-151026/15.  
DR  
XX  
XX  
PT Detecting target nucleic acid (T) using probe, comprises amplifying  
PT target sequence (S) so that end of (S) which is hybridized with probe is  
PT positioned at less than 40 bases from terminal base of (T) and detecting  
PT hybridization with probe.  
XX  
XX  
PS Disclosure; SEQ ID NO 22; 47pp; Japanese.  
XX  
CC The invention comprises a method for detecting a target nucleic acid. The  
CC method of the invention is useful for: single nucleotide polymorphism  
CC detection, diagnosis of disease by analysing disease-related genes,  
CC estimating risk of incidence of the disease, detection of infection,  
CC analysing virus types, and in toxicity studies. The present nucleic acid  
CC represents a human MxA gene DNA sequence which was used in the  
CC exemplification of the invention.  
XX  
SQ Sequence 581 BP; 120 A; 147 C; 213 G; 100 T; 0 U; 1 Other;  
Query Match 87.6%; Score 18.4; DB 12; Length 581;  
Best Local Similarity 90.5%; Pred. No. 1.2e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GCAAGTGTCTAGGTGCGGG 21  
DB 410 GCAAGTGTCTAGGTGCGGG 430  
RESULT 29  
ADL92269  
ID ADL92269 standard; DNA; 581 BP.  
XX  
AC ADL92269;  
XX  
XX 20-MAY-2004 (first entry)  
XX  
DE Human MxA gene DNA sequence #7.  
XX  
XX nucleic acid detection; immobilised nucleic acid probe;  
KW single nucleotide polymorphism detection; SNP detection;  
KW disease diagnosis; ds; human; MxA gene.  
XX  
OS Homo sapiens.  
XX  
PN JP2004041109-A.  
XX  
PD 12-FEB-2004.  
XX  
PF 12-JUL-2002; 2002JP-00204444.  
XX  
XX 12-JUL-2002; 2002JP-00204444.  
XX  
PA (TOKE ) TOSHIBA KK.  
XX  
XX WPI; 2004-151026/15.  
DR  
XX  
XX  
PT Detecting target nucleic acid (T) using probe, comprises amplifying  
PT target sequence (S) so that end of (S) which is hybridized with probe is  
PT positioned at less than 40 bases from terminal base of (T) and detecting  
PT hybridization with probe.  
XX  
XX  
PS Disclosure; SEQ ID NO 26; 47pp; Japanese.  
XX  
CC The invention comprises a method for detecting a target nucleic acid. The  
CC method of the invention is useful for: single nucleotide polymorphism  
CC detection, diagnosis of disease by analysing disease-related genes,  
CC estimating risk of incidence of the disease, detection of infection,

CC analysing virus types, and in toxicity studies. The present nucleic acid  
CC represents a human MxA gene DNA sequence which was used in the  
CC exemplification of the invention.  
XX  
SQ Sequence 581 BP; 119 A; 147 C; 213 G; 101 T; 0 U; 1 Other;  
Query Match 84.8%; Score 17.8; DB 12; Length 581;  
Best Local Similarity 90.5%; Pred. No. 2.2e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GCAAGTGTCTAGGTGCGGG 21  
DB 410 GCAAGTGTCTAGGTGCGGG 430  
RESULT 30  
ADL92268  
ID ADL92268 standard; DNA; 581 BP.  
XX  
AC ADL92268;  
XX  
XX 20-MAY-2004 (first entry)  
XX  
XX Human MxA gene DNA sequence #6.  
XX  
XX nucleic acid detection; immobilised nucleic acid probe;  
KW single nucleotide polymorphism detection; SNP detection;  
KW disease diagnosis; ds; human; MxA gene.  
XX  
OS Homo sapiens.  
XX  
PN JP2004041109-A.  
XX  
PD 12-FEB-2004.  
XX  
PF 12-JUL-2002; 2002JP-00204444.  
XX  
PR 12-JUL-2002; 2002JP-00204444.  
XX  
PA (TOKE ) TOSHIBA KK.  
XX  
XX WPI; 2004-151026/15.  
DR  
XX  
XX  
PT Detecting target nucleic acid (T) using probe, comprises amplifying  
PT target sequence (S) so that end of (S) which is hybridized with probe is  
PT positioned at less than 40 bases from terminal base of (T) and detecting  
PT hybridization with probe.  
XX  
XX  
PS Disclosure; SEQ ID NO 25; 47pp; Japanese.  
XX  
XX The invention comprises a method for detecting a target nucleic acid. The  
XX method of the invention is useful for: single nucleotide polymorphism  
XX detection, diagnosis of disease by analysing disease-related genes,  
XX estimating risk of incidence of the disease, detection of infection,  
XX analysing virus types, and in toxicity studies. The present nucleic acid  
XX represents a human MxA gene DNA sequence which was used in the  
XX exemplification of the invention.  
XX  
SQ Sequence 581 BP; 118 A; 148 C; 214 G; 100 T; 0 U; 1 Other;  
Query Match 84.8%; Score 17.8; DB 12; Length 581;  
Best Local Similarity 90.5%; Pred. No. 2.2e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GCAAGTGTCTAGGTGCGGG 21  
DB 410 GCAAGTGTCTAGGTGCGGG 430  
RESULT 31  
ABL34192  
ID ABL34192 standard; DNA; 5981 BP.  
XX

AC ABL34192;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Human immune system associated gene SEQ ID NO: 2165.  
XX  
KW Human; immune system disease; cytosine methylation; antiasthmatic;  
XX antiarteriosclerotic; anianaemic; cytosatic; nootropic;  
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmologic;  
KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;  
KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;  
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;  
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;  
KW ds.  
XX  
OS Homo sapiens.  
XX  
XX WO200200928-A2.  
PN  
XX 03-JAN-2002.  
PD  
XX  
XX 02-JUL-2001; 2001WO-EP007537.  
PF  
XX  
XX 30-JUN-2000; 2000DE-01032529.  
PR  
XX 01-SEP-2000; 2000DE-01043826.  
PR  
XX (EPIG-) EPIGENOMICS AG.  
PA  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2002-130909/17.  
PI  
XX Nucleic acid comprising fragment of chemically modified gene, useful for  
PT diagnosis and treatment of diseases associated with abnormal cytosine  
PT methylation.  
PT  
XX Claim 1; SEQ ID NO 2165; 32pp + Sequence Listing; German.  
PS  
XX  
XX The present invention provides a number of human immune system associated  
CC genes which are modified by the methylation of cytosines. The sequences  
CC can be used in the diagnosis and treatment of immune system disorders,  
CC including eye diseases such as retinopathy, neovascular glaucoma and  
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid  
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,  
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel  
CC diseases. The present sequence is a gene of the invention  
CC  
XX Sequence 5981 BP; 1433 A; 174 C; 1715 G; 2659 T; 0 U; 0 Other;  
SQ  
Query Match 84.8%; Score 17.8; DB 6; Length 5981;  
Best Local Similarity 90.5%; Pred. No. 2.7e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 GCAAGTCTGTAGTGGGG 21  
Db 4867 GTAAGTCTGTAGTGGGG 4887  
RESULT 32  
ABL70483  
ID ABL70483 standard; DNA; 5981 BP.  
XX  
XX ABL70483;  
AC  
XX  
XX 01-JUL-2002 (first entry)  
DT  
XX Chemically treated cell signalling DNA sequence#187.  
DE  
XX Cell signalling; cytosine methylation; cell signalling disease; cancer;  
KW tumour; cytosatic; ds.  
KW  
XX Unidentified.  
OS  
XX

PN WO200202807-A2.  
XX  
PD 10-JAN-2002.  
XX  
XX 29-JUN-2001; 2001WO-EP007471.  
PF  
XX  
XX 30-JUN-2000; 2000DE-01032529.  
PR  
XX 01-SEP-2000; 2000DE-01043826.  
PR  
XX (EPIG-) EPIGENOMICS AG.  
PA  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2002-154758/20.  
PI  
XX Nucleic acid, useful for diagnosis and therapy of diseases associated  
PT with cell signaling e.g. cancer, comprises chemically modified genomic  
PT sequences of genes associated with cell signaling.  
PT  
XX Claim 1; SEQ ID NO 373; 24pp + Sequence Listing; English.  
PS  
XX  
XX The invention relates to a nucleic acid comprising a sequence of at least  
CC 18 bases of a segment of chemically pretreated DNA of genes associated  
CC with cell signalling. The activity of the modified sequences of the  
CC invention may be described as cytostatic. The object of the invention is  
CC to provide the chemically modified DNA of genes associated with cell  
CC signalling, as well as oligonucleotides and/or PNA-oligomers for  
CC detecting cytosine methylations, as well as a method which is  
CC particularly suitable for the diagnosis and/or therapy of genetic and  
CC epigenetic parameters of genes associated with cell signalling. The  
CC chemically modified DNA provided by the invention is useful for diagnosis  
CC and therapy of diseases such as solid tumours and cancer. The sequences  
CC given in records ABL70111-ABL70626 represent chemically pre-treated  
CC genomic DNA's of genes associated with cell signalling. Note: The  
CC sequence data for this patent is not represented in the printed  
CC specification, but is based on sequence information supplied by the  
CC European Patent Office  
XX  
XX Sequence 5981 BP; 1433 A; 174 C; 1715 G; 2659 T; 0 U; 0 Other;  
SQ  
Query Match 84.8%; Score 17.8; DB 6; Length 5981;  
Best Local Similarity 90.5%; Pred. No. 2.7e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 GCAAGTCTGTAGTGGGG 21  
Db 4867 GTAAGTCTGTAGTGGGG 4887  
RESULT 33  
ABL69125/c  
ID ABL69125 standard; DNA; 3302 BP.  
XX  
XX ABL69125;  
AC  
XX  
XX 15-MAY-2002 (first entry)  
DT  
XX  
XX Kidney cancer related gene sequence SEQ ID NO:7462.  
DE  
XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;  
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;  
KW cytosatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;  
KW gene; ds.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200194629-A2.  
PN  
XX 13-DEC-2001.  
PD  
XX 30-MAY-2001; 2001WO-US010838.  
XX  
XX 05-JUN-2000; 2000US-0209473P.  
PR

PR 05-JUN-2000; 2000US-0209531P.  
 PR 18-SEP-2000; 2000US-0233133P.  
 PR 18-SEP-2000; 2000US-0233617P.  
 PR 20-SEP-2000; 2000US-0234009P.  
 PR 20-SEP-2000; 2000US-0234034P.  
 PR 20-SEP-2000; 2000US-0234052P.  
 PR 22-SEP-2000; 2000US-0234509P.  
 PR 22-SEP-2000; 2000US-0234567P.  
 PR 25-SEP-2000; 2000US-0234923P.  
 PR 25-SEP-2000; 2000US-0234924P.  
 PR 25-SEP-2000; 2000US-0235077P.  
 PR 25-SEP-2000; 2000US-0235082P.  
 PR 25-SEP-2000; 2000US-0235134P.  
 PR 25-SEP-2000; 2000US-0235280P.  
 PR 26-SEP-2000; 2000US-0235637P.  
 PR 26-SEP-2000; 2000US-0235638P.  
 PR 27-SEP-2000; 2000US-0235711P.  
 PR 27-SEP-2000; 2000US-0235840P.  
 PR 27-SEP-2000; 2000US-0235863P.  
 PR 28-SEP-2000; 2000US-0236028P.  
 PR 28-SEP-2000; 2000US-0236032P.  
 PR 28-SEP-2000; 2000US-0236033P.  
 PR 28-SEP-2000; 2000US-0236034P.  
 PR 28-SEP-2000; 2000US-0236109P.  
 PR 28-SEP-2000; 2000US-0236111P.  
 PR 29-SEP-2000; 2000US-0236842P.  
 PR 29-SEP-2000; 2000US-0236891P.  
 PR 02-OCT-2000; 2000US-0237172P.  
 PR 02-OCT-2000; 2000US-0237173P.  
 PR 02-OCT-2000; 2000US-0237278P.  
 PR 02-OCT-2000; 2000US-0237295P.  
 PR 02-OCT-2000; 2000US-0237316P.  
 PR 03-OCT-2000; 2000US-0237425P.  
 PR 03-OCT-2000; 2000US-0237598P.  
 PR 03-OCT-2000; 2000US-0237604P.  
 PR 03-OCT-2000; 2000US-0237606P.  
 PR 03-OCT-2000; 2000US-0237608P.  
 PR 01-NOV-2000; 2000US-0244867P.  
 PR 01-NOV-2000; 2000US-0245084P.  
 PA (AVAL-) AVALON PHARM.  
 XX  
 XX  
 PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;  
 PI Soppet DR, Weaver Z;  
 XX  
 XX  
 DR WPI; 2002-188264/24.  
 XX  
 PT Screening for anti-neoplastic agent involves exposing cells to a chemical  
 PT agent to be tested for anti-neoplastic activity, and determining a change  
 PT in expression of a gene of a signature gene set.  
 XX  
 XX  
 PS Claim 1; SEQ ID NO 7462; 44pp; English.  
 XX  
 CC The present invention describes a method (M1) for screening for an anti-  
 CC neoplastic agent. The method involves exposing cells to a chemical agent  
 CC to be tested for anti-neoplastic activity, determining a change in  
 CC expression of at least one gene (I) of a signature gene set, where (I)  
 CC comprises a sequence (S) selected from 8447 sequences (given in ABU6164  
 CC to ABL70110), or is at least 95% identical to (S), where a change in  
 CC expression is indicative of anti-neoplastic activity. (I) has cytostatic  
 CC activity and can be used in gene therapy. M1 can be used for screening an  
 CC anti-neoplastic agent, and can be used for producing a product which is  
 CC of M1, and the data is sufficient to convey the chemical structure and/or  
 CC properties of the agent. M1 can be used in the treatment of cancer such  
 CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,  
 CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell  
 CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous  
 CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms'  
 CC tumour  
 XX

SQ Sequence 3302 BP; 852 A; 865 C; 788 G; 797 T; 0 U; 0 Other;  
 Query Match 81.0%; Score 17; DB 6; Length 3302;  
 Best Local Similarity 100.0%; Pred. No. 5,9e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 GTGCTGTAGTGGCGGG 21  
 DB 541 GTGCTGTAGTGGCGGG 525  
 RESULT 34  
 ADRI4356/c  
 ID ADRI4356 standard; DNA; 3302 BP.  
 XX  
 AC ADR14356;  
 XX  
 DT 21-OCT-2004 (first entry)  
 XX  
 DE Human NF-kappaB pathway-associated gene SeqID357.  
 XX  
 KW NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;  
 KW antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic;  
 KW antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;  
 KW immunosuppressive; vulnary; gene therapy; immune disorder;  
 KW inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;  
 KW hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;  
 KW hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;  
 KW X-linked anhidrotic ectodermal dysplasia; immunodeficiency;  
 KW viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;  
 KW viral replication; host cell survival; evasion of immune response;  
 KW rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;  
 KW atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;  
 KW autoimmune disorder; hyper immune activity;  
 KW aberrant acute phase response; hypercongenital condition; birth defect;  
 KW necrotic lesion; wound; organ transplant rejection;  
 KW aberrant signal transduction; proliferating disorder; cancer;  
 KW HIV propagation; gene; ds; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004065577-A2.  
 XX  
 PD 05-AUG-2004.  
 XX  
 PF 13-JAN-2004; 2004WO-US0000798.  
 XX  
 PR 14-JAN-2003; 2003US-0440068P.  
 PR 12-MAY-2003; 2003US-0469757P.  
 XX  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 XX  
 PI Nadler SG, Neubauer MG, Feder JN, Carman J;  
 XX  
 DR WPI; 2004-562168/54.  
 DR P-PSDB; ADRI4357.  
 XX  
 PT New isolated polynucleotides and polypeptides associated with NF-kappaB  
 PT pathway, useful for diagnosing, treating, or preventing disorders or  
 PT diseases associated with NF-kappaB pathway.  
 XX  
 PS Claim 1; SEQ ID NO 357; 237pp; English.  
 XX  
 CC This invention relates to the novel association of protein sequences (and  
 CC the genes which encode them) to the NF-kappaB pathway. The invention may  
 CC be useful for the production of compounds with an antiinflammatory,  
 CC cytostatic, hepatotropic, virucide, antiarthritic, antirheumatic,  
 CC gastrointestinal-Gen, antiasthmatic, antiarteriosclerotic,  
 CC immunomodulator, cerebroprotective, vasotropic, immunosuppressive or  
 CC vulnary activity or for gene therapy. The proteins and nucleotides are  
 CC useful for diagnosing, preventing, treating, or ameliorating conditions  
 CC or diseases associated with the NF-kappaB pathway. The condition is an  
 CC immune disorder, an inflammatory disorder, an inflammatory disorder

CC related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,  
 CC hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM  
 CC syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic  
 CC syndromal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,  
 CC hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell  
 CC survival, evasion of immune responses, rheumatoid arthritis, inflammatory  
 CC bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick  
 CC syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper  
 CC immune activity, disorders related to aberrant acute phase responses,  
 CC hypercongenital conditions, birth defects, necrotic lesions, wounds,  
 CC organ transplant rejection, conditions related to organ transplant  
 CC rejection, disorders related to aberrant signal transduction,  
 CC proliferating disorders, cancers and HIV propagation in cells infected  
 CC with other viruses. The present sequence is that of a human gene which is  
 CC subject to the novel association with the NF-kappaB pathway of the  
 CC invention. Note: This sequence does not appear in the specification but  
 CC was obtained by the indexer from Genbank.

XX  
 XX Sequence 3302 BP; 852 A; 865 C; 788 G; 797 T; 0 U; 0 Other;  
 Query Match 81.0%; Score 17; DB 13; Length 3302;  
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGGG 21  
 |||||  
 Db 541 GTGCTGTAGTGGGG 525

RESULT 35  
 ADX07310/c  
 ID ADX07310 standard; DNA; 3302 BP.  
 AC ADX07310;  
 XX  
 XX 21-APR-2005 (first entry)  
 DT  
 XX  
 XX Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 1875.  
 DE  
 XX  
 XX cytostatic; cyclin-dependent kinase; cdk; biomarker; gene; ds.  
 KW  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO2005012875-A2.  
 PN  
 XX  
 XX 10-FEB-2005.  
 PD  
 XX  
 XX 29-JUL-2004; 2004WO-US024424.  
 PF  
 XX  
 XX 29-JUL-2003; 2003US-0490890P.  
 PR  
 XX  
 XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 PA  
 XX  
 XX Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;  
 PI  
 XX P-PSDB; ADX07311.  
 DR  
 XX  
 XX WPI; 2005-163068/17.  
 DR  
 XX

PT Biomarkers useful for predicting or determining the response of a mammal  
 PT to a cancer treatment comprising administration of a modulator of cyclin-  
 PT dependent kinase activity.  
 PT  
 XX  
 XX Claim 5; SEQ ID NO 1875; 141pp; English.

CC This invention describes a novel method of predicting or determining  
 CC whether a mammal will respond or is responding to an anti-cancer agent  
 CC that modulates cyclin-dependent kinase (cdk) activity. The method  
 CC comprises measuring the level of one or more biomarkers selected from  
 CC 2774 biomarkers given in the specification (nucleotide sequence SEQ ID  
 CC NO.1246 (Genbank EST W28729) is especially preferred). The method of the  
 CC invention is utilized in a kit for determining or predicting whether  
 CC patient would be susceptible or resistant to treatment by an agent  
 CC modulating cdk activity. The invention also describes a method for

CC utilizing individualized genetic profiles for treating diseases and  
 CC disorders based on patient's response and molecular level, specialized  
 CC microarrays comprising the biomarkers described, antibodies directed  
 CC against the biomarkers and a cell culture model to identify biomarkers.  
 CC The cdk modulator is preferably N-5-[(5-(1,1-Dimethylethyl)-2-  
 CC oxazolyl)methylthio]-2-thiazolyl-4-piperidine carboxamide, 0.5-L-  
 CC tartaric acid salt. Note: The sequence data for this patent did not form  
 CC part of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pst\_sequences. This  
 CC sequence encodes a biomarker used in the method of the invention.  
 XX  
 XX Sequence 3302 BP; 852 A; 865 C; 788 G; 797 T; 0 U; 0 Other;

Query Match 81.0%; Score 17; DB 14; Length 3302;  
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGGG 21  
 |||||  
 Db 541 GTGCTGTAGTGGGG 525

RESULT 36  
 ADZ49006/c  
 ID ADZ49006 standard; DNA; 3302 BP.  
 AC ADZ49006;  
 XX  
 XX 30-JUN-2005 (first entry)  
 DT  
 XX  
 XX Insulin signaling pathway related gene, SEQ ID 335.  
 DE  
 XX  
 XX Antidiabetic; Gene Therapy; Non-insulin dependent diabetes;  
 KW  
 XX Insulin resistance; gene; ds.  
 XX  
 XX Homo sapiens.  
 OS  
 XX US2005085436-A1.  
 FN  
 XX 21-APR-2005.  
 PD  
 XX  
 XX 08-JUL-2004; 2004US-00887553.  
 PF  
 XX  
 XX 08-JUL-2003; 2003US-0485883P.  
 PR  
 XX  
 XX (LIHH/) LI H.  
 PA (MAJJ/) MA J.  
 PA  
 XX  
 XX Li H, Ma J;  
 PI  
 XX WPI; 2005-305194/31.  
 DR

PT Treating, preventing or ameliorating pathological conditions associated  
 PT with dysregulation of the insulin signaling pathway (ISP) comprises  
 PT administering to a subject an amount of a modulator of any of the  
 PT proteins regulated by ISP.  
 PT  
 XX  
 XX Disclosure; SEQ ID NO 335; 70pp; English.

XX The present invention relates to a method for treating, preventing or  
 XX ameliorating pathological conditions associated with dysregulation of the  
 XX insulin signaling pathway (ISP). The method comprises administering to a  
 XX subject a modulator for ISP-regulated proteins or a pharmaceutical  
 XX composition comprising the described modulator. The method is useful for  
 XX treating, preventing or ameliorating pathological conditions associated  
 XX with dysregulation of the ISP such as Type II diabetes or Type A syndrome  
 XX of insulin resistance. The present sequence is a human homolog of a  
 XX Drosophila gene regulated by ISP. Note: The sequence data for this patent  
 XX did not form part of the printed specification, but was obtained in  
 XX electronic format directly from USPTO at  
 XX seqdata.uspto.gov/sequence.html?docID=20050085436.

XX Sequence 3302 BP; 852 A; 865 C; 788 G; 797 T; 0 U; 0 Other;



```
Query Match      81.0%; Score 17; DB 14; Length 3302;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGCGGG 21
DB 541 GTGCTGTAGTGGCGGG 525

RESULT 37
ACN90319/c
ID AEB56452 standard; cDNA; 3302 BP.
XX
AC AEB56452;
XX
AD 20-OCT-2005 (first entry)
XX
DE Radiochemotherapy response detection associated cDNA SEQ ID NO 27.
XX
KW gene expression; chemotherapy; radiotherapy; prognosis; diagnosis;
KW adenocarcinoma; cytostatic; neoplasm; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2005073411-A1.
XX
PD 11-AUG-2005.
XX
PF 12-JAN-2005; 2005WO-US000891.
XX
PR 12-JAN-2004; 2004US-0535491P.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Ried T, Difilippantonio MJ, Ghadimi B, Grade M, Becker H;
PI Liersch T;
XX
DR WPI; 2005-555710/56.
DR P-PSDB; AEB56509.
XX
XX New compositions having isolated nucleic acids, polypeptides and
PT antibodies, useful for diagnosing, detecting radiochemotherapy response
PT and prognosticating rectal adenocarcinomas.
XX
PS Claim 16; SEQ ID NO 27; 266pp; English.
XX
CC The invention describes a composition comprising at least 5 isolated
CC nucleic acids of at least 15 contiguous nucleotides selected from nucleic
CC acids that correspond to genes 1-54 from any of 54 significantly changed
CC genes in class comparison analysis, given in the specification as Table
CC 3, and comprising no more than 9000 total isolated nucleic acids. The
CC methods and compositions of the present invention are useful for
CC diagnostic and research applications, in particular for diagnosing,
CC detecting radiochemotherapy response and prognosticating rectal
CC adenocarcinomas. This sequence represents a cDNA the expression of which
CC is altered in rectal adenocarcinoma cells.
XX
SQ Sequence 3302 BP; 852 A; 865 C; 788 G; 797 T; 0 U; 0 Other;

Query Match      81.0%; Score 17; DB 14; Length 3302;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGCGGG 21
DB 541 GTGCTGTAGTGGCGGG 525

RESULT 38
ACN90319/c
ID ACN90319 standard; DNA; 3579 BP.
XX

ACN90319;
XX
DT 02-DEC-2004 (first entry)
XX
DE Breast cancer related marker, seq id 11469.
XX
KW Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
XX
OS Homo sapiens.
XX
PN US2003099974-A1.
XX
PD 29-MAY-2003.
XX
PF 18-JUL-2002; 2002US-00198846.
XX
PR 18-JUL-2001; 2001US-0306220P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Lillie J, Xu Y, Wang Y, Steinmann K;
XX
DR WPI; 2003-787014/74.
XX
XX Novel isolated polypeptide associated with breast cancer, useful for
PT detecting presence of polypeptide in sample, as a marker for breast
PT cancer.
XX
PS Disclosure; SEQ ID NO 11469; 36pp; English.
XX
CC The invention relates to an isolated polypeptide (I) associated with
CC breast cancer which is encoded by a nucleic acid molecule comprising a
CC nucleotide sequence (S1). Further disclosed is an antibody that binds to
CC the polypeptide of the invention. The activity of the polypeptide of the
CC invention may be described as cytostatic. The antibody is useful for
CC detecting the presence of (I) in a sample. Nucleic acid molecules of the
CC invention are useful in the detection of breast tumours. (I) is useful as
CC a marker for breast cancer and in breast cancer therapy. Sequences given
CC in records ACN78851-ACN92934 represent nucleic acid markers associated
CC with breast cancer. Note: The sequence listing does not form part of the
CC specification but may be obtained in electronic format from the USPTO web
CC site at seqdata.uspto.gov/sequence.html?docID=20030099974
XX
SQ Sequence 3579 BP; 900 A; 929 C; 867 G; 862 T; 0 U; 21 Other;

Query Match      81.0%; Score 17; DB 11; Length 3579;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTGCTGTAGTGGCGGG 21
DB 628 GTGCTGTAGTGGCGGG 612

RESULT 39
ACF74962
ID ACF74962 standard; DNA; 633 BP.
XX
AC ACF74962;
XX
DT 20-NOV-2003 (first entry)
XX
DE Staphylococcus aureus DNA #2642.
XX
KW Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
KW enzymatic assay; antibiotic target; gene; ds.
XX
OS Staphylococcus aureus.
XX
PN WO200294868-A2.
XX
PD 28-NOV-2002.
XX
```

PF 27-MAR-2002; 2002WO-IB002637.  
XX  
PR 27-MAR-2001; 2001GB-00007661.  
XX  
PA (CHTR-) CHIRON SPA.  
XX  
PI Masignani V, Mora M, Scarselli M;  
XX  
PI WPI; 2003-120786/11.  
XX  
DR P-PSDB; ABW73402.  
XX  
XX New Staphylococcus aureus protein, useful as a vaccine for treating or  
PT preventing Staphylococcal infection, specifically an infection caused by  
PT S. aureus, e.g. sepsis.  
XX  
XX Claim 6; SEQ ID NO 5283; 49pp; English.  
PS  
XX The invention relates to novel genes and encoded proteins from  
CC Staphylococcus aureus. A composition comprising the S. aureus protein, a  
CC nucleic acid encoding the protein, or an antibody to the protein, is  
CC useful as a pharmaceutical, particularly as a vaccine for treating or  
CC preventing infection due to Staphylococcus bacteria, specifically an  
CC infection caused by S. aureus. The composition is particularly useful for  
CC treating or preventing sepsis in a patient. The composition can also be  
CC used for diagnostics. The protein is also used in an assay for enzymatic  
CC studies and as a target for antibiotics. This sequence represents one of  
CC the novel S. aureus genes of the invention  
XX  
SQ Sequence 633 BP; 183 A; 97 C; 132 G; 221 T; 0 U; 0 Other;  
Query Match 80.0%; Score 16.8; DB 8; Length 633;  
Best Local Similarity 90.0%; Pred. No. 6.5e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GCAAGTGTCTAGTGGCGG 20  
DB 457 GCAAGTTATGTAGTGGCGG 476  
RESULT 40  
AAS93751/c  
ID AAS93751 standard; cDNA; 954 BP.  
XX  
XX AAS93751;  
XX  
DT 13-FEB-2002 (first entry)  
XX  
XX DNA encoding novel human diagnostic protein #29555.  
XX  
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200175067-A2.  
XX  
XX 11-OCT-2001.  
XX  
XX 30-MAR-2001; 2001WO-US008631.  
XX  
XX 31-MAR-2000; 2000US-00540217.  
PR  
XX 23-AUG-2000; 2000US-00649167.  
XX  
XX (HYSE-) HYSEQ INC.  
PA  
XX Drmanac RT, Liu C, Tang YT;  
XX  
XX WPI; 2001-639362/73.  
DR  
XX P-PSDB; ABG29564.  
XX  
XX New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess

PT biodiversity.  
XX  
PS Claim 1; SEQ ID NO 29555; 103pp; English.  
XX  
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging  
CC of sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activity. The  
CC polypeptide and polynucleotide sequences have application in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic  
CC coding sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 954 BP; 215 A; 283 C; 267 G; 189 T; 0 U; 0 Other;  
Query Match 80.0%; Score 16.8; DB 5; Length 954;  
Best Local Similarity 90.0%; Pred. No. 6.7e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GCAAGTGTCTAGTGGCGG 20  
DB 210 GTAACTGCTGTAGTGGCGG 191  
RESULT 41  
AAS81868/c  
ID AAS81868 standard; cDNA; 1840 BP.  
XX  
XX AAS81868;  
XX  
XX 13-FEB-2002 (first entry)  
XX  
XX DNA encoding novel human diagnostic protein #17672.  
XX  
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200175067-A2.  
XX  
XX 11-OCT-2001.  
XX  
XX 30-MAR-2001; 2001WO-US008631.  
XX  
XX 31-MAR-2000; 2000US-00540217.  
PR  
XX 23-AUG-2000; 2000US-00649167.  
XX  
XX (HYSE-) HYSEQ INC.  
PA  
XX Drmanac RT, Liu C, Tang YT;  
XX  
XX WPI; 2001-639362/73.  
DR  
XX P-PSDB; ABG17681.  
XX  
XX New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.

BS Claim 1; SEQ ID NO 17672; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)

CC sequences. (I) is useful as hybridisation probes, polymerase chain

CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping.

CC and in recombinant production of (II). The polynucleotides are also used

CC in diagnostics as expressed sequence tags for identifying expressed

CC genes. (I) is useful in gene therapy techniques to restore normal

CC activity of (II) or to treat disease states involving (II). (II) is

CC useful for generating antibodies against it, detecting or quantitating a

CC polypeptide in tissue, as molecular weight markers and as a food

CC supplement. (II) and its binding partners are useful in medical imaging

CC of sites expressing (II). (I) and (II) are useful for treating disorders

CC involving aberrant protein expression or biological activity. The

CC polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations

CC responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and

CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic

CC coding sequences of the invention. Note: The sequence data for this

CC patent did not appear in the printed specification, but was obtained in

CC electronic format directly from WIPO at

XX ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 1840 BP; 413 A; 513 C; 525 G; 389 T; 0 U; 0 Other;

Query Match 80.0%; Score 16.8; DB 5; Length 1840;

Best Local Similarity 90.0%; Pred. No. 7e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGTCCGG 20

DB 210 GTAAGTGTCTAGTGTCCGG 191

RESULT 42

AAD01353/c

ID AAD01353 standard; cDNA; 1972 BP.

XX AC AAD01353;

XX DT 12-OCT-2000 (first entry)

XX DE Wheat sphingolipid desaturase cDNA #1.

XX KW Wheat; sphingolipid desaturase; membrane-bound desaturase;

XX KW transgenic plant; fatty acid; ss.

XX OS Triticum aestivum.

XX FH Key Location/Qualifiers

FT CDS 124..1533

FT /\*tag= a

FT /product= "Sphingolipid desaturase"

XX WO200032790-A2.

XX PN 08-JUN-2000.

XX PD 02-DEC-1999; 99WO-US028589.

XX PR 03-DEC-1998; 98US-0110784P.

XX PA (DUPO) DU PONT DE NEMOURS & CO E I.

XX PI Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ;

XX DR WPI; 2000-412336/35.

XX DR P-FSDB; AAY71555.

XX PT Polynucleotide encoding delta-6 desaturase enzyme useful for producing

XX PT transgenic plants and for producing antibodies specific to which is

XX PT useful for screening cDNA expression libraries.

XX PS Disclosure; Page 48-49; 57pp; English.

XX The present sequence is a cDNA encoding sphingolipid desaturase from

CC clone wrel.pk004.c7.fis isolated from wheat etiolated seedling root cDNA

CC library, wrel. The present sequence is useful for producing transgenic

CC plants having altered levels of sphingolipid desaturase which in turn

CC would alter the fatty acid composition. The enzyme is useful for

CC producing polyclonal or monoclonal antibodies. The polynucleotide is also

CC useful as primer or probe for screening cDNA libraries to isolate desired

CC full-length cDNA clones

XX SQ Sequence 1972 BP; 382 A; 616 C; 490 G; 484 T; 0 U; 0 Other;

Query Match 80.0%; Score 16.8; DB 3; Length 1972;

Best Local Similarity 90.0%; Pred. No. 7.1e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGTCTAGTGTCCGG 20

DB 829 GCAAGTGTCTAGTGTCCGG 810

RESULT 43

AAS81864/c

ID AAS81864 standard; cDNA; 2178 BP.

XX AC AAS81864;

XX DT 13-FEB-2002 (first entry)

XX DE DNA encoding novel human diagnostic protein #17668.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR P-FSDB; AEG17677.

XX PT New isolated polynucleotide and encoded polypeptides, useful in

XX PT diagnostics, forensics, gene mapping, identification of mutations

XX PT responsible for genetic disorders or other traits and to assess

XX PT biodiversity.

XX PS Claim 1; SEQ ID NO 17668; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)

CC sequences. (I) is useful as hybridisation probes, polymerase chain

CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,

CC and in recombinant production of (II). The polynucleotides are also used

CC in diagnostics as expressed sequence tags for identifying expressed

CC genes. (I) is useful in gene therapy techniques to restore normal

CC activity of (II) or to treat disease states involving (II). (II) is

CC useful for generating antibodies against it, detecting or quantitating a

CC polypeptide in tissue, as molecular weight markers and as a food

CC supplement. (II) and its binding partners are useful in medical imaging

CC of sites expressing (II). (I) and (II) are useful for treating disorders

CC involving aberrant protein expression or biological activity. The

CC polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic  
 CC coding sequences of the invention. Note: The sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 2178 BP; 481 A; 626 C; 632 G; 439 T; 0 U; 0 Other;  
 Query Match 80.0%; Score 16.8; DB 5; Length 2178;  
 Best Local Similarity 90.0%; Pred. No. 7.1e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 GCAAGTGTCTAGGTGCGGG 20  
 Db 1623 GTAACGTCTAGGTGCGGG 1604  
 RESULT 44  
 AAS89697/c  
 ID AAS89697 standard; cDNA; 2179 BP.  
 XX  
 AC  
 AC AAS89697;  
 DT 13-FEB-2002 (first entry)  
 XX  
 DE DNA encoding novel human diagnostic protein #25501.  
 XX  
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 XX  
 PF 30-MAR-2001; 2001WO-US008631.  
 XX  
 PR 31-MAR-2000; 2000US-00540217.  
 PR 23-AUG-2000; 2000US-00649167.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Drmanac RT, Liu C, Tang YT;  
 XX  
 DR WPI; 2001-639362/73.  
 DR P-PSDB; ABG25510.  
 XX  
 PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.  
 XX  
 PS Claim 1; SEQ ID NO 25501; 103pp; English.  
 XX  
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 CC sequences. (I) is useful as hybridisation probes, polymerase chain  
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations

CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic  
 CC coding sequences of the invention. Note: The sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 2179 BP; 481 A; 627 C; 632 G; 439 T; 0 U; 0 Other;  
 Query Match 80.0%; Score 16.8; DB 5; Length 2179;  
 Best Local Similarity 90.0%; Pred. No. 7.1e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 GCAAGTGTCTAGGTGCGGG 20  
 Db 1623 GTAACGTCTAGGTGCGGG 1604  
 RESULT 45  
 AAS93754/c  
 ID AAS93754 standard; cDNA; 2250 BP.  
 XX  
 AC  
 AC AAS93754;  
 DT 13-FEB-2002 (first entry)  
 XX  
 DE DNA encoding novel human diagnostic protein #29558.  
 XX  
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 XX  
 PF 30-MAR-2001; 2001WO-US008631.  
 XX  
 PR 31-MAR-2000; 2000US-00540217.  
 PR 23-AUG-2000; 2000US-00649167.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Drmanac RT, Liu C, Tang YT;  
 XX  
 DR WPI; 2001-639362/73.  
 DR P-PSDB; ABG29557.  
 XX  
 PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.  
 XX  
 PS Claim 1; SEQ ID NO 29558; 103pp; English.  
 XX  
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 CC sequences. (I) is useful as hybridisation probes, polymerase chain  
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and

CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic  
CC coding sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 2250 BP; 505 A; 615 C; 628 G; 502 T; 0 U; 0 Other;  
Query Match 80.0%; Score 16.8; DB 5; Length 2250;  
Best Local Similarity 90.0%; Pred. No. 7.1e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GCAAGTGTCTAGGTGCGGG 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 663 GTAACGTCTGTAGGTGCGGG 644  
RESULT 46  
AAS93758/c  
ID AAS93758 standard; cDNA; 2830 BP.  
XX  
AC AAS93758;  
XX  
DT 13-FEB-2002 (first entry)  
XX  
DE DNA encoding novel human diagnostic protein #29562.  
XX  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2001WO-US008631.  
XX  
PR 31-MAR-2000; 2000US-00540217.  
XX  
PR 23-AUG-2000; 2000US-00649167.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Drmanac RT, Liu C, Tang YT;  
XX  
DR WPI; 2001-639362/73.  
XX  
DR P-PSDB; ABG29571.  
XX  
PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.  
XX  
PS Claim 1; SEQ ID NO 29562; 103pp; English.  
XX  
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a  
CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging  
CC of sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activity. The  
CC polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC polypeptide and polynucleotide sequences have applications in  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic  
CC coding sequences of the invention. Note: The sequence data for this

CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 2830 BP; 599 A; 761 C; 884 G; 586 T; 0 U; 0 Other;  
Query Match 80.0%; Score 16.8; DB 5; Length 2830;  
Best Local Similarity 90.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GCAAGTGTCTAGGTGCGGG 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1965 GTAACGTCTGTAGGTGCGGG 1946  
RESULT 47  
AAS93339/c  
ID AAS93339 standard; cDNA; 3039 BP.  
XX  
AC AAS93339;  
XX  
DT 13-FEB-2002 (first entry)  
XX  
DE DNA encoding novel human diagnostic protein #29143.  
XX  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2001WO-US008631.  
XX  
PR 31-MAR-2000; 2000US-00540217.  
XX  
PR 23-AUG-2000; 2000US-00649167.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Drmanac RT, Liu C, Tang YT;  
XX  
DR WPI; 2001-639362/73.  
XX  
DR P-PSDB; ABG29152.  
XX  
PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.  
XX  
PS Claim 1; SEQ ID NO 29143; 103pp; English.  
XX  
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a  
CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging  
CC of sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activity. The  
CC polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC polypeptide and polynucleotide sequences have applications in  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic  
CC coding sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at

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CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 3039 BP; 658 A; 790 C; 883 G; 708 T; 0 U; 0 Other;
Query Match 80.0%; Score 16.8; DB 5; Length 3039;
Best Local Similarity 90.0%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTGCTGTAGTGCGGG 20
   ||| ||||| ||||| |||||
Db 2829 GTAACGCTGTAGTGCGGG 2810

RESULT 49
AAS93240
ID AAS93240 standard; cDNA; 3039 BP.
XX
AC AAS93240;
XX
XX 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #29044.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX P-PSDB; ABG29053.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX
PS Claim 1; SEQ ID NO 25465; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX and in recombinant production of (II). The polynucleotides are also used
XX in diagnostics as expressed sequence tags for identifying expressed
XX genes. (I) is useful in gene therapy techniques to restore normal
XX activity of (II) or to treat disease states involving (II). (II) is
XX useful for generating antibodies against it, detecting or quantitating a
XX polypeptide in tissue, as molecular weight markers and as a food
XX supplement. (II) and its binding partners are useful in medical imaging
XX of sites expressing (II). (I) and (II) are useful for treating disorders
XX involving aberrant protein expression or biological activity. The
XX polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
XX coding sequences of the invention. Note: The sequence data for this
XX patent did not appear in the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX

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Query Match 80.0%; Score 16.8; DB 5; Length 3039;  
 Best Local Similarity 90.0%; Pred. No. 7.3e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 GCAAGTGTCTAGTGGGG 20  
 Db 457 GAACTGTCTAGTGGGG 476  
 Search completed: January 27, 2006, 05:44:40  
 Job time : 222.5 secs

RESULT 50  
 AAS85756  
 ID AAS85756 standard; cDNA; 3355 BP.  
 XX  
 AC .AAS85756;  
 XX  
 DT 13-FEB-2002 (first entry)  
 XX  
 DE DNA encoding novel human diagnostic protein #21560.  
 XX  
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200175067-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 30-MAR-2001; 2001WO-US008631.  
 XX  
 PR 31-MAR-2000; 2000US-00540217.  
 PR 23-AUG-2000; 2000US-00649167.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Drmanac RT, Liu C, Tang YT;  
 XX  
 DR WPI; 2001-639362/73.  
 DR P-PSDB; ABG21569.  
 XX  
 PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.  
 XX  
 PS Claim 1; SEQ ID NO 21560; 103pp; English.  
 XX  
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 CC sequences. (I) is useful as hybridisation probes, polymerase chain  
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (II) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic  
 CC coding sequences of the invention. Note: The sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 3355 BP; 714 A; 964 C; 897 G; 780 T; 0 U; 0 Other;

Query Match 80.0%; Score 16.8; DB 5; Length 3355;  
 Best Local Similarity 90.0%; Pred. No. 7.3e+02;

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